

# STIC Search Report Biotech-Chem Library

# STIC Dalabase Tracking (Number

TO: Sheridan Swope

**Art Unit: 1656** 

Location: rem/2B71/3C70 Serial Number: 09/940235

Friday, February 03, 2006

From: Beverly Shears

**Location: Biotech-Chem Library** 

**REM 1A54** 

Phone: 571-272-2528

beverly.shears@uspto.gov

# Search Notes

### Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

### **Published Applications Database - November 2005**

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_New).



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From: Sent: Subject: Swope, Sheridan

Thursday, January 26, 2006 3:36 PM STIC-Biotech/ChemLib

RE: 09/940,235

PLEASE ALSO ALIGN SID 9, 10, 11, AND 12. Thanks!

----Original Message-----

Sent:

Swope, Sheridan

Wednesday, January 25, 2006 8:28 PM STIC-Biotech/ChemLib

09/940,235 Subject:

For 09/940,235, pls search:

SID 9 against the NT and AA databases

NA 1541

SID 10 against the NT and AA databases NA 166(

SID 11 against the NT and AA databases NA 1982

NA 2096 SID 12 against the NT and AA databases

Sheridan Swope, Ph.D. Patent Examiner, AU 1656 Recombinant Enzymes 571-272-0943 (voice) E02B71 Remsen Bld (Office) E03C70 Remsen Bld (Mailbox)

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

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NA#	AA#:
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09/940235 Page Seg, 1059-12

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> 0 < O | O IntelliGenetics . 0 ^ GENALIGN - Multiple Sequence Alignment Program Release 5.4

Thu 2 Feb 106 9:25:14-PST

Solution Parameters:

= Identity = 0ff = Off = Off AMINO-Res-length = 2
DELetion-weight = 5.00
LEngth-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
SPread-factor = 50 Nucleic Alphabet = Output line length = Compress = Histogram = Randomization = =

Clustered order of selected sequences:

(1-1541) (1-1661) (1-1782) (1-2096) . US-09-940-235-9 . US-09-940-235-10 . US-09-940-235-11 . US-09-940-235-12 

Region Alignment: (listed in Clustered order)

US-09-940-US-09-940-

US-09-940-US-09-940cgaagaccattcatgttgttgctcaggtcgcagacgttttgcagcagcagtcgcttcacgt consensus

US-09-940-

1 12 TCGCTCGCGTATCGGTGATTCTGCTAACCAGTAAGGCAACCCGCCAGCCTAGCCGG US-09-940-US-09-940-

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GCAACCCCGCCAGCCTAGCCGG

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GTCCTCAACGACCACCACCACCACCCCCAGGCCCAACCCAACGCTGCCCGAGA gtcctcaacgacaggagcacgatcatgcgcacccgtggccaggacccaacgctgcccgaga 123 consensus US-09-940-

US-09-940-

134 US-09-940-US-09-940-

US-09-940- 361 CTGATCGAAACGCAAGGTCTACTTGCTGACAAAGATGGTTCGGTAACCTTGCCGACCCA

184 TCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGA  tctcgatcccgcgaaattaatacgactcactatagggagaccacaacggtttccctctaga  1	S6   AGALCGTCCTTGTAAAAACAGCCAATTGGTTGTTAGCGTTGCTGGTACTGTTGAGGGG		178 GAGGAAAGACAAGGCTTAAGTCCAAATCAAAACCATTTGCTACTGATAGTGGGGC	239 GATGTCACATAAACTTGAGAAAGCTGACTTACTAAAGGCTATTCAAGAACAATTGATCGCT  389 GATGTCACATAAACTTGAGAAAGCTGACTTACTAAAGGCTATTCAAGAACAATTGATCGCT  389 GATGTCACAAAACTTGAGAAAAGCTGACTTACTAAAGGCTATTCAAGAAATTGATGCT  439 TGCATCTGCACAGCAACGGCCAACAGGCTGGAAGTTGTAGTAGAAGACACCTCTGTTGTAAAATTGATGAAAAAAAA	300 AACGTCCACAGTAACGACGACTACTTTGAGGTCATTGCAAGCGATGCCAACCATTA
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US-09-940- US-09-940- US-09-940- consensus	511 CTGATCG 561 AGACCGG [       611 AGACCGG	CTGATCGAAACGGCAAGGTCTACTTGCTGACAAAGATGGTTCGGTAACCTTGCCGACCCA AGACCGTCCATCTGTCAACAACAGCCAATTGGTTGCTTGC
US-09-940- US-09-940- US-09-940- US-09-940- consensus	422 ACCTGT               572 ACCTGT           622 ACGAAT 672 ACGAAT	ACCTGTCCAAGAATTTTTGCTAAGCGGACATGTGCGCGTTAGACCATTTAAAGAAAAACCA ACCTGTCCAAGAATTTTTGCTAAGCGGACATGTGCGCGTTAGACCATTAAAAGAAAAACCA
US-09-940- US-09-940- US-09-940- US-09-940- CONSENBUS	483 ATACAAA               633 ATACAAA     683 GAGGAAA 733 GAGGAAA	ATA CAAAA CCAAGGGAAAT CTGTTGATGTGGAATA TACTGTACAGTTTACTCCCTTAAACC ATA CAAAAA CCAAGGGAAAT CTGTTGTGGAATA TACTGTACAGTTTACTCCCTTAAACC ATA CAAAAA CCAAGGGAAT CTGTTGTGGAATA TACTGTACAGTTTACTCCCTTAAACC AGGAAAGACCAGGCTAAGCTTAAGTCCAAAAT CCAAAACCATTTGCTACTGATAGTGGGC GAGGAAAGACAGGCTTAAGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGC GAGGAAAGACAGGCTTAAGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGC GAGGAAAGACAGGCTTAAGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGC CAAAAAACAAAAAAAAAA
US-09-940- US-09-940- US-09-940- US-09-940- CONSENBUS	544 CTGATGACG [	CTGATGACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGG CTGATGACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGG CTGATGACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGG
US-09-940- US-09-940- US-09-940- US-09-940- CONSENBUS	605 TGACACCAT            755 TGACACCAT     805 AACGTCCAC           855 AACGTCCAC	TGACACCATCACAACAAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAACCAC
US-09-940- US-09-940- US-09-940- US-09-940- consensus	666 CCAGGC 816 CCAGGC               866 CTGATO 916 CTGATO	CCAGGCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTTCC CCAGGCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACATTTTCC CCAGGCTAAACGATTTATGAACGTGACTCCTCCAATCATCATCAATCA
US-09-940- US-09-940- US-09-940- US-09-940-	727 GTACGA 	

CTGATGACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGG US-09-940- 1232 GTACGATTTACCAATGGATCAAGAGTTTACTTACTTAAGAATGGGGAACAAGAGCTTA US-09-940- 1282 GTACGATTTACCAATGGATCAAGAGTTTAACTTACCGTGTTAAAAATCGGGAACAAGCTTA US-09-940- 1282 GTACGATTTACCAATGGATCAAGAGTTTAACTTAACGGGTTAAAAATCGGGAAAAACTAA TAGGATCAATAAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCTCTGAG AAATATTACGTCCTTAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCGTCACTTGA AAATATTACGTCCTTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGA --AC-A-T-TAC-A----TC-A---TTT---TA---TG----A-A-C---A----TAG----A--A--AT----C-----A--A-A-----TG--C-----C---US-09-940- 1354 AAATATTÄCGTČCTTAAAAAAGGGGAAAAAGCCGTATGATCCČTTTGATCGCAGTCACTTGA -------T---A-C-C---C-T-G-849 666 1049 1099 971 1221 US-09-940- 1343 US-09-940- 1293 US-09-940- 1121 US-09-940- 1171 US-09-940-US-09-940-US-09-940-US-09-940-US-09-940-US-09-940-US-09-940-US-09-940-US-09-940-US-09-940consensus consensus US-09-940consensus consensus consensus

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cAgTcccCGgtggCTGtcAgTcaaAgcaaGcCcggtTgTtATGaCaAtGgAAaacaCtAtc US-09-940- 1404 AAATATTACGTCCTTAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGA A-----A---C----Aa-A----a-G--GT--g----C---g--c--aGTc-cttga gctgagaaGtgtttTGatcaTgctggGaCttccTaTgtgGtCggaGaAAcgtgggAga AACTGTTCACCATCAAATACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCT AACTGTTCACCATCAAATACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCT aactgttc-ccatc--atac-ttgatgtcGa-acca-c-aat-gCtaa-aA-tgagca-ct AGccctAcCAAggcTGGatGatGgtagAttgtacTtgccTGggagGaagGcAgcgGacgcat AGatAaAtCAAcaGTGGGaGCGGacctAcctAGgTAaTgTGttGCTttGtActtGttatgg CTTAACAGCTAGCGAACGTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCT CITAACAGCTAGCGAACGTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCT --taacAgC-Agcg---gt-ac-taga-ttcaga-attt--acg-tcc-c-tga-aaggct US-09-940- 1337 cacttGCacttcTagaAAtaGatgcAacgAtCagGAcaCaaggacatCcTatagaattgga . AggaaGCcgaaggTtttAACiGcgaaAgTaAaCctGAAgCtgaagagaCTTgctTtGAcAAG AAACTACTACAACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAG aaact-Ctctac-acaA-ct-gatg-ttt-g-ta--at-gactatacCtTaactggaaag US-09-940- 1398 gACACctGGAgCAagaAggataatcGaGgaAacctgctcCagtgcAtctgCaCaggcAaCg tA-A-ga--AtCAcga-gacaccaa-cGta-cataaccg-ttata-gggc-a-cgac-c-a US-09-940- 1459 GccgagGagagTGgAagtGtGagaGGGacacctctgTgcagaccACatcgagcggatctgg . US-09-940- 1709 AGGAGAGAATGCTACCTACCATTTAGCtggtggTggccaggcGcaacagATtgtacccAta -ggagaGaatg--a-ctagc-ttt-GC--g-g-tagtaa-gagcacc-tatac-ga-ca-g cTAtgAtaaaGatCgtTATAccgaagAag US-09-940- 1609 GGGActGtAccTGcAtcgGGGCTgGGCgagggagAaTAagctGtACcaTcTAa TAGAGGATAATCACGATGACACCAACCGTATCATAACCG 1659 AGGAGAATGCTAGCTAtCATTTAGC cccttcaccgatgttcgttag 1215 1365 1465 US-09-940- 1415 US-09-940- 1476 1487 US-09-940- 1587 US-09-940- 1548 US-09-940- 1598 US-09-940- 1276 US-09-940- 1426 US-09-940- 1526 US-09-940- 1537 US-09-940- 1520 US-09-940- 1662 US-09-940-US-09-940-US-09-940-US-09-940consensus consensus US-09-940consensas consensus

US-09-940- 1831 agccctaccaaggctggatgatggtagattgtacttgcctgggagaaggcAGCggacgcat cacttgcacttctagaaatagatgcaacgatcaggacacaaaggacatcctatagaattgga cacttgcacttctagaaatagatgcaacgatcaggacacaaggacatcctatagaattgga agccctaccaaggctggatgatggtagattgtacttgcctgggaga---cagcggacgcat US-09-940- 1953 gacacctggagcaagaaggataatcgaggaaAccTGctccagtgcatcTgcAcAcGaacg gacacctggagcaagaaggataatcgagga-acctgctccagtgca--t--acaggcaacg 2014 gccgaggagagtggaagtgtgagaggcACACCTctgtgcagaccacatcgagcggaTctgg gccgaggagagtggaagtgtgagagg-acacctctgtgcagaccacatcga----t----JS-09-940- 2075 cCCTtcaccgAtgTtcgttag US-09-940- 1766 aCCCTaacgacAaaTaa 1892 US-09-940- 1725 US-09-940- 1662 US-09-940- 1732 US-09-940- 1542 US-09-940- 1662 US-09-940- 1732 US-09-940- 1542 US-09-940- 1542 US-09-940- 1662 US-09-940- 1749 US-09-940- 1662 US-09-940- 1542 US-09-940consensus consensus consensus consensus consensus

US-09-940- 1770 gctGAGAAGTgttttgatcatgctgctgggacttcctatgtggtcggagaaacgtgggaga

US-09-940- 1715 aacGAGAAGT

-ccgagaagtg-t-t----gctgctgggacttcctatgtggtcggagaaacgtgggaga

US-09-940- 1542

= -2900.00

Alignment score

Scoring matrix:

113215 Sequence 45,20030 SEQ ID NO:
113219 Sequence 46,20021 SEQ ID NO:
113209 Sequence 34,368315 Streptococc AX1360315 Sequence AX030315 Sequence AX030316 Sequence AX030316 Sequence AX030318 Sequence AX030318 Sequence AX030318 Sequence AX030318 Sequence AX030318 Sequence 39,113205 Sequence 39,13206 Sequence 30,13206 Sequence 30,13206

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Sequence:

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270 CTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAG 329
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Bacterial fibrin-dependent plasminogen activator
Bacterial fibrin-dependent plasminogen activator
Patent: US 6210667-A 1 03-APR-2001;
Location/Qualifiers
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1 from patent US 6210667.
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10524 Sequence 5
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A04926 S.equisimil
X72813 S.equisimil
X72812 S.equisimil
X7087820 Sequence
AR068768 Sequence
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A20015 SEQ ID NO:
113203 Sequence 25
R01413 DNA Sequence
A20016 SEQ ID NO:
113204 Sequence
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A20016 SEQ ID NO:
113197 Sequence 27
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SEQ ID NO:
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362 TTGCTGACAAGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGAATTTTTGCTAA 421   445 GCGGACATGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTG 504   1		STRSKC STRSKC STRSKC STRSKC STRSKC STRSKC STRSKC STRPPLOPOUS STREPLOCOCCUS equisimilis (H46A) streptokinase gene, complete cds. ACCESION VERSION KO2986.1 GI:153808 KEYMORDS Streptococcus dysgalactiae subsp. equisimilis STREPTOCOCCUS dysgalactiae subsp.
B41 GAAAAGCCGTATGCTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 900   933 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCGAACGTAAC 992	105204	Oy         145 TTGAAATCGATCTAACATCACGACCTGCTCATGGAGAAGACAGGCAAGGCTTAAGTC         204           Db         122 TTGAAATCGATCTCAACGACCTGCTCATGGAGGAAGGCAAGGCTTAAGTC         181           Oy         205 CAAAATCAAAACCATTTGCTACTGATAGTGGCGCATGTCACTAAACTTGAGAAAGCTG         264           Db         182 CAAAATCAAAACCATTTGCTACTGATAGTGGCGCATGTCACATAAACTTGAGAAAGCTG         241           Oy         265 ACTTACTAAAGGCTATTCAAGAACAATTGATGGCCAAGTCCACAGTAACGACGACTACT         324           Db         242 ACTTACTAAAGGCTATTTGAAACAATTGATCGCTAACGTCCACAGTAACGACGACTACT         301           Oy         325 TTGAGGTCATTTGAAAGAACAATCGAACCATTACTGATCGAAACGCCAAGGTCTACT         301           Oy         325 TTGAGGTCATTTGAAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACT         361           Db         302 TTGAGGTCATTTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACT         361           Oy         325 TTGAGGTCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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                                                                                                                                                                                  GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
Bacteria, Pirmicutes, Lactobacillales, Streptococcaceae,
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1 (bases 1 to 2568)

1 cerretti, J. J. and Malke, H.

Streptokinase-coding recombinant vectors
Patent: EP 015137-A 1 14-AUG-1985;
THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
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/mol_type="unassigned DNA"
/sub_species="equisimlis"
/db_xref="texon:119602"
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Draft entry and hard copy of sequence for [1] kindly provided by J.J.Ferretti, 0.-SEP-1985.

The -35 and -10 regions are located at positions 760-765 and 781-786 respectively and an SD sequence at 808-813. Downstream from the coding region inverted repeats (positions 2176-2190 and 2203-2217) are thought to function as transcription terminators. The nucleotide sequence of skc does not support the hypothesis that the gene has evolved by duplication and fusion, as suggested by internal two-fold AA homologies of its product.

Location/Qualifiers

1. .2568

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Anologies of its product.

Anologies of its product.
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0; Mismatches 14;
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/note="prestreptokinase"

/codon start=1

/transT_table=11

/protein_id="AAA26974.1"

/db_xref="GI:153809"
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/product="streptokinase"
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/product="8kc mRNA"
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Best Local Similarity 98.8%;
Matches 1141; Conservative
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pMF1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Streptococcus dysgalactiae subsp. equisimilis"
/mol_type="genomic DNA"
/strain="H46A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (05-MAY-1993) H. Malke, Institute for Molecular Biology,
Jena University, Winzerlaer Str 10, 07708 Jena, FRG
Related sequences: K02986, M19346, X13399 & X13400.
                                                                                                                                                                                                                                                            glucan
                                                                                                                                                                                                                                       X72832.1 GI:407876

abc gene; ABC transporter; dexB gene; dextran glucosidase; glucar l,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel gene; skc gene; streptokinase; stringent response-like protein. Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
                                                                                                                                                                                                                                                                                                                                                 Streptococcus.

1 (bases 3621 to 6190)

Malke, H., Roe, B. and Ferretti, J.J.

Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description of the Albert of the Exception of the Streptochinase region of the Streptococcus equisimilis H6A chromosome Mol. Gen. Genet. 241 (1-2), 129-140 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:119602"
/chromosome="streptokinase region"
/clone_lib="s.coli plasmid library containing
pcwp73, pRH10, pwX4"
complement (89. .1761)
                                                                                                                                                                                               DNA linear Borel genes and ORF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /isolate="human group C strain"
/sub_species="equisimilis"
                                                                                                                                                                                            S.equisimilis dexb, abc, lrp, skc, X72832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hairpin loop"
complement (136. .1749)
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2989113
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complement (89. .115)
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/transl_table=
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/EC_number=".
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                                                             GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCCAAAATCA
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                                                                                                                                                                GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGGCAAGGCTTAAGTCCAAAATCA
                                                                                                                                                                                                                                                                                    AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC
                                                                                                                                                                                                                                                                                                          1137 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGAGAACGACGACTACTTTGAGGTC
                                                                                                                                                                                                                                                                                                                                             ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
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                 Gaps
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               Indels
                  14;
 Pred. No. 3.1e-278;
0; Mismatches 14;
 98.88;
Best Local Similarity
Matches 1141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product; ORF1"
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                                                                                                                       .
4172. .4368
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4392. .5837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="streptokinase"
                        complement (4141. .4146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6317. .8536)
/gene="rel"
                                                                 .4149)
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                                                                                                                                                                                                                                                                                                                                                                         /note="alternative"
1428. .4431
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                                                                                                                                                                                                                                                                                                                                                                                                                                         4439. .5761
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                                                             complement (4148.
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                                                                                                            'note="TG motif"
                                                                                                                                                                                                                                                                 note="TG motif"
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6162. .6164
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                                                                                                                                                                                                                    4392. .4393
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5796. .5837
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/gene="skc"
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                        -10_signal
                                                                                                                                                                                                                                                                                        -10_signal
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HTSDEHAWFVEARENPNSPERDYYIWRDEPNNLMSIFSGSAWELDEASGOYYLHLFSK
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complement (4117. .4120)
                                                                                                                                                                                                                                                                                   /gene="abc"
/note="hairpin loop"
complement(2482, .2499)
                                                                                                                                                                                                                    complement (1780. .3051)
                                                                                                                                                                                                                                                                                                                                                 /gene="abc"
/note="Walker motif B"
complement(2633. .2965)
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complement (3244. .4149)
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                                                                                                                                                                         complement (1757. .1761)
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complement(2973. .2976)
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Db 5597 ACCAACCGTATCATAACCGTTTATATGGGCAAGGGACCCGAAGGAGAATGCTAGCTA	ITION DNA fragment of plasmid PMP1 into which DNA encoding stris in inserted.  SION E0652.  BO0522.1 GI:2168801  NDS P1985237995-A/1.  RDS Streptcoccus dysgalactiae subsp. equisimilis  R Streptcoccus dysgalactiae subsp. equisimilis  ANISM Streptcoccus dysgalactiae subsp. equisimilis  Bacteria; Firmicutes, Lactobacillales, Streptcoccaeae,		58 (7)	CC *source: library=streptococcus equismilis H46A; CC *source: clone=lambda L47 skc clone; FH Key Location/Qualifiers FT S'UTR 1. 818 FT sig_peptide 819896 FT mat_peptide 8972138 FT Store Streptokinase signal peptide FT	FT CDS /product='Bireprokinase' FT 3'UTR 2143. 2569. FEATURES 1.0.2568 1.0.2568 /mol_type="genomic DNA" /mol_type="genomic DNA	Query Match         73.2%;         Score 1127.8;         DB 6;         Length 2568;           Best Local Similarity 98.5%;         Pred. No. 5.2e-277;         Accessory of the second of the sec
		333 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAAGGCAAGGTCTACTTTGCTGAC 392	GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGTTGTTGTG 499 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGAATTTCAGACCAGGTCTCAAA 572 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 572 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 505 GATACTAAGCTATTGAAAACACTAGGTGATGGCGACACATCACAACAACTACTAA 632	5057 GAIACIAAGCIAITGAAAACAACIAICGGIGAACCATCACATCTCAGGAATTACIA 5116 633 GCTCAAGCACAAAGCATTTAAACAAAAACCACGGGCTATACGATTATGAACGTGC 692 6117 GCTCAAGCACAAAGCATTTTAAACAAAAACACCCCAGGCTATACGATTATGAACGTGAC 5176 693 TCCTCAATCGTCACTCATGACAATGACAATTACCGTACGATTTACCAATGGATCAAGGG 752 6177 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGG 5236 5177 TCCTCAATCGTCATCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGG 5236	753 5237 813 5297 873	\$357 GAAAAGCCGTATGATCACCTTGAACCTTCACCATCAATACGTT 5416  \$33 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCACCATCAAATACGTT 5416  \$33 GATGTCGATACCAACGAATTGCTAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 992  \$417 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTAACAGCTAACGGAACGTAAC 5476  \$93 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACACAATCTC 1052  \$111

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                                                                                  selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D. and ramos gonz Lez,O.
vector for the production of transplastomic angiosperm plants Patent: WO 2004,02955A 26 08-APR-20104;
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                                                                                                                                                                        /organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Nucleotide
sequence of DNA fragment from the vector pVTPA-Estrep
between the rice atpB and tobacco rbcL borders."
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                                                             other sequences; artificial sequences
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                                                AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC
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linear

CQ797820 7057 bp DN Sequence 26 from Patent WO2004029256.

CQ797820 LOCUS DEFINITION

RESULT

Oy         273 AAGSCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC         332           Db         1135 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACTACTTTGAGGTC         1194           Oy         333 ATTGATTTTGCAAGCGATGCAATCGATCGAAACGGCAAGGTCTACTTTGCTGAC         392           Db         1195 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAACGGCAAGGTCTACTTTGCTGAC         1254           Oy         393 AAAGATGGTTGGGTAGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC         1254           Db         11255 AAAGATGGTTCGGTAACCTTGCCCAACCTGTCCAAGAATTTTTGCTAAGCGAAT         452           Db         1255 AAAGATGGTTCGGTAACCTTGCCGACCTGTCCAAGAATTTTTGCTAAGCGGACAT         1314	Qy         453 GTGGGGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGGGAAATCTGTTGATGT 512           Db         1315 GTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGGGAAATCTGTTGATGT 1374           Qy         513 GAATATACTGTACACTTTACTCCCTTAAACCCATTTCACACCACCACCCACAAA 572           Db         1375 GAATATACTGTACACTTTAATCCCTTAAACCCTGATGACAATTCAAACCAACTCTCAAA	GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA	OY 633 GCTCAAGCACAAACCATTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 692	OY 693 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 752	Oy 753 TTTACTTACCGTGTTAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 812  1615 TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 1674  OY 813 AATGAAGAATAAACAACTGACCTGGTCTCTGAGAAATATACGTCCTTAAAAAAGGG 872	873 GAAAAGCCGTATGATCCCTTTGATCGCGGTCACTTGAAACTGTTCACCATCAAATACGTT	QY         933 GATGTCGAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC         992	1855 TIAGACITCAGAGAITTATACGATCCTCGTGATAAGGCTAAACTACTCTCAGAGAATCTCTC	Qy 1053 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGATAATCACGATGAC 1112	OY 1113 ACCAACGTATCATAACGGTTTATATGGGCAAGCGACCCGAAGGAGAGAGA	Oy 1173 CATTAGCTGGTCGT 1187 	RESULT 10 S46536 S46536 1245 bp DNA linear BCT 08-MAY-1993 DREFINITION SKC-2-strentplinase [Strentpording equisinile groun C and Color	Genomic, 1245 nt]. 846536 846536.1 GI:257196
Qy         743 GGATCAAGAGTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAA         802           Db         2733 GGATCAAGAGTTTACTTACCATGTCAAAAATCGGGAACAAGCTTATGAGATCAATAAAAA         2792           Qy         803 ATCTGGTCAATGAAGAAATAAACAACAGACTGACTGACTG	Qy         923 CAAATACGTTGATGTCGATACCAACTACTGAAAAGTGAGCAGCTCTTAACAGCTAG 982           Db         2913 CAAATACGTTGATGTCAACACGAATTGCTAAAAAGCGAGCTGCTTAACAGCTAG 2972           Qy         983 CGAACGTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGCTAAACTACTCTA         1042           Db         2973 CGAACGTAACTTCAGAGATTTATACGATCCTCGTGATAAGCTAAACTACTCTA         3032	Qy 1043 CAACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGATAA 1102 	QY     1103 TCACGATGACCCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAA 1162       T	Qy 1163 TGCTAGCTACCATTAGCTGGTGGT 1187  Db 3153 TGCTAGCTATCATTAGCCTATGAT 3177	RESULT 9 AR068768 LOCUS AR068768 DEFINITION Sequence 19 from patent US 5854049, VERSION AR068768 USES 10 GI:6000975	Unknown. Unknown. Unclassified	eed, G.L. lasmin-resista atent: US 5854 Locati		, Query Match 72.6%; Score 1118.6; DB 6; Length 2566; Best Local Similarity 98.6%; Pred. No. 1.2e-274; Matches 1139; Conservative 0; Mismatches 14; Indels 2; Gaps 1;	CCTGAATGGCTACTAGATCGTCCTTCTGTAAATAACAGCCAATTGGTTGTT 92		OY 153 GATCTAACATCACGACCTGCTCATGGAAAAGACAGAGCATAAGTCCAAAATCA 212	OY 213 AAACCATTTGCTACTGATGGGGGGATGTCACATAAACTTGAGAAAGCTGACTTACTA 272 

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TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAATCTC 1020
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 GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAATCAAGCGAAATCTGTTGATGTG 480
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                                 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACAACTCTCAAGAATTACTA
                                                                                                                                                                         GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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23; Nucleotide sequence for
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1 (bases 1 to 1257)
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Patent: WO 9109125-A 23 27-JUN-1991;
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LLYNNLDAFGIMDYTLTGKVEDNHDDTNRIITVYMGKRPEGENASYHLAYDKDRYTEE

EREVYSYLRYTGTPIPDNPNDK"
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                                                                                                                                                                                                                                                                           /organism="Streptococcus dysgalactiae subsp. equisimilis"
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Estrada,M.P., Hernandez,L., Perez,A., Rodriguez,P., Serrano,R.,
Rubiera,R., Pedraza,A., Padron,G., Antuch,W., de la Fuente,J. et
                                                                                                                                                                                                                                                                                                                                                                                                                    Met"
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                                                                                                                                                                                                       GenBank staff at the National Library of Medicine created thi
entry [NCBI gibbsq 115306] from the original journal article.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                /note="streptokinase; Mature protein lacks initial /codon_start=1
                                                                                                                                                  High level expression of streptokinase in Escherichia coli
Biotechnology (N.Y.) 10 (10), 1138-1142 (1992)
1368792
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Pred. No. 6.5e-273;
0; Mismatches 27; Indels 0;
              Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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larity 97.7%;
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Dawson, K., Hunter, M.G. and Czaplewski, L.G.
Pibrinolytic and anti-thrombotic cleavable dir
Patent: US 5434073-A 25 18-UUL-1995,
Location/Qualifiers

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/db.xref="GI:1247484"
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PR 24-DEC-1987
PP 02-MAY-1986 US 86
PR 08-MAY-1986 US 8
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/mol_type="genomic DNA"
/db_xref="taxon:4081"
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Lycopersicon esculentum (Solanum lycopersicum)
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Elycopersicon esculentum
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
ascerids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1407)
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EFLLSGHVRVRPYKEKPIQNQAKSVDVEYTVQFTPLNPDDDFRPGLKDTKLLKTLAIG
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TVYMGKRPEGENASYHLAYDKDRYTEERREVYSYLRYTGTPIPDNENDK"
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for streptokinase fused to yeast
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                                                  ATCAAGAGTTTACTTACGGTGTTAAAATCGGGAACAAGCTTATAGGATCAATAAAAAT 804
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                                                                                                                                                                                                           AATACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCG 984
                                                                                                   CTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTA
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7. .1506
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Patent: WO 9109125-A 24 27-JJN-1991;
Location/Qualifiers
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SEQ 1b NO: 24; Nucleotide sequence
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AAAAAGGGGAAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCA 1153
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ACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATC
            1274 ACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAAGATAATC
                                                    ACGATGACACCAACCGTATCATAACCGTTTTATATGGGCAAGCGACCCGAAGGAGAATG
                                                                    25 ATACCATGATAGCTGGTCCTGAATGGCTACTAGATCGTCCTTCTGTAAATAACAGCCAAT
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                                                                                                                                                                                                    linear
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1 (bases 1 to 1512)
5 Dawson, K., Hunter, M.G. and Czaplewski, L.G.
Fibrinolytic and anti-thrombotic cleavable dim
L Patent: US 5434073-A 27 18-JUL-1995;
L Location/Qualifiers
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US 5434073
                                                                                                                           CTAGCTATCATTTAGCCTATGAT 1416
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Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a chimeric streptkinase-fibrin binding domain (SK-PBD) protein coding sequence. The invention relates to a hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sahni G, Kumar R, Roy C, Rajogopal K, Nihalani D,
Yadav M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus dysgalactiae subsp. equisimilis.
Homo sapiens.
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                                                                                                                                                                                                                                                                                     AAQ10230
AAX80494
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ADS17488
              AAQ12162
AAQ12490
AAQ12160
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ADW44479
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AAN50493
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AAX80493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric SK-FBD coding sequence.
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AAA3764
  Aaa37644 Chimeric
Aaa37643 Chimeric
Aaa37628 Streptoki
Aaa37622 Streptoki
Aaa37622 Chimeric
Aax80497 Streptoki
Aad1651 FB-FB-SK
Aax80492 Streptoki
Aad1651 FB-FB-SK
Aax80492 Streptoco
Aax16632 Streptoki
Aba05546 Streptoki
Aba05547 Maxadilan
Aax16632 Streptoco
Adm01294 Plasmid p
Aax17778 Coding se
Aar7778 Coding se
Aar7778 Streptoki
Aax16633 Streptoco
Adm01294 Plasmid p
Aax17778 Coding se
Aar7778 Coding se
Aar7778 Coding se
Aar7778 Streptoki
                                                                                          January 31, 2006, 10:44:08; Search time 931.565 Seconds (without alignments) 11024.772 Million cell updates/sec
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                                                                                                                                                                                                                                                                                    9993994
           GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                   nucleic search, using sw model
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Score

Result

96

Sundaram V;

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fireptokinase (SK), which are capable of planinogen (EG) activation, and fibrin binding regions of human fibronectin, which are from fibrin binding regions of human fibronectin, which are from fibrin ability to bind with fibrin independently and also characteristically retains a FG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human FG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinnetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of
                                                                                                                                                                                                                                                                                                                                                                                                                       plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen to plasmin, thus aiding in the localisation of the plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
   comprises a polypeptide fusion between
   plasminogen activator (PA)
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Sequence 1541 BP; 497 A; 328 C; 335 G; 381 T; 0 U; 0 Other;

120 180 180 240 240 300 300 360 420 420 480 480 540 540 900 999 99 ACCACCCAGGCTATACGATTTATGAACGTGACTCCTCAATCGTCACCATCATGACAATGACA 720 GTCCTTCTGTAAATAACAGCCAATTGGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGA 120 ACGTCCACAGTAACGACGACTACTTTGAGGTCATTGATTTTGCAAGCGATGCAACCATTA 360 900 9 ATCAAGACATTAGTCTTAAATTTTTTGAAATCGATCTAACATCACGACCTGCTCATGGAG ATCAAGACATTAGTCTTAAATTTTTTGAAATCGATCTAACATCAGGACCTGCTCATGGAG TGTCACATAAACTTGAGAAAGCTGACTTACTAAAAGGCTATTCAAGAACAATTGATCGCTA AACCTGTCCAAGAATTTTTGCTAAGCGGACATGTGCGCGTTAGACCATATAAAGAAAAAC CAATACAAAACCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAA TCGGTGACACCATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAA TGTCACATAAACTTGAGAAAGCTGACTTACTAAAGGCTATTCAAGAACAATTGATCGCTA CAATACAAAACCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAA TCGGTGACACCATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAA TTTGTTTAACTTTAAGAAGGAGATATACCATGATAGCTGGTCCTGAATGGCTACTAGATC TTTGTTTAACTTTAAGAAGAGAGATATACCATGATAGCTGGTCCTGAATGGCTACTAGATC GTCCTTCTGTAAATAACAGCCAATTGGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGA GAAAGACAGAGCAAGGCTTAAGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGCGA GAAAGACAGAGCAAGGCTTAAGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGCGA CTGATCGAAACGCCAAGGTCTACTTTGCTGACAAAGATGGTTCGGTAACCTTGCCGACCC AACCTGTCCAAGAATTTTTGCTAAGCGGACATGTGCGCGTTAGACCATATAAAGAAAAC **ACCCTGATGACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTA** ACGTCCACAGTAACGACGACTACTTTGAGGTCATTGATTTTGCAAGCGATGCAACCATTA CTGATCGAAACGCCAAGGTCTACTTTGCTGACAAAGATGGTTCGGTAACCTTGCCGACCC Gaps ö DB 3; Length 1541; Indels , 0 100.0%; Score 1541; 100.0%; Pred. No. 0; tive 0; Mismatches Conservative Best Local Similarity Matches 1541; Conserv Н 121 121 241 301 541 541 601 561 61 181 361 421 421 481 481 Query Match 61 181 241 301 501 361 셤 8 셤 g ò g ያ ዓ 品 格 格 谷 g ઠે र्घ कि र्घ ò 음 장

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ò	781	AAGCTTATAGGATCAATAAAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGA 840
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දු දු	841	TCTCTGAGAAATATTACGTCCTTAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCA 900 
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දි දි	961 (	GTGAGCAGCTCTTAACAGCTAGCGAACGTAACTTAGACTTCAGAGATTTATACGATCCTC 1020 
ò	1021	GIGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTTCGTATTATGGACTATACCT 1080
qq	1021 (	JIGATAAGGCTAAACTACTACAACAATCTCGATGCTTTTGGTATTATGGACTATACCT 1080
È	1081	TAACTIGGAAAAGTTAGAGATAATCACGATGACCAACCGTATCATAACCGTTTTATATIGG 1140
셤	1081	raactggaaaagtagaggataatcacgatgacaccaaccgtatcataaccgtttatatggg 1140
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Š	1201	AGATIGIACCCAIAGCIGAGAAGIGITITGAICAIGCIGCIGGGGACITCCIAIGIGGICG 1260
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ð	1501 (	CCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTTAG 1541
qq	1501	CACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTTAG 1541
RESUI AAA3' ID	2 .3 .A37643	standard; DNA; 2096 BP.
X Z i	AAA37643;	
<b>*</b> 5 5 5	-SEP-20	03 (revised) 00 (first entry)
<b>名</b> 图 \$	imeric	SK-PBD coding sequence.
KW St KW D1	Streptoki plasminog cardiovas	Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy; cardiovascular disorder; ss.

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                                             TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
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                                                                                                                                       AAAGATGGTTCGGTAACCTTGCCGACCCTGTCCAAGAATTTTTGCTAAGCGGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1488 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1548 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGCTTTTGGTATTATGGACTATACCTTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTTAGCTGGTGGCCCAGGCGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTTAGCTGGTGGTGGCCAGGCGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGCTGCTGGGACTTCCTATGTGGTCGGAGAACGTGGGAGAGGCCCTACCAAGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAAGCCCTACCAAGGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAGATGCAACGATCAGGACACACAGGACATCCTATAGAATTGGAGACACCTGGAGCAAG
                                                                                           888
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Pred. No. 0;
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Best Local Similarity 98.8%;
Matches 1194; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SK; hybrid plasminogen activator; fibrin binding region; man; fibronectin; thrombolytic therapy;
GTGAGCAGCTCTTAACAGCTAGCGAACGTAAACTTAGACTTCAGAGATTTATACGATCCTC
                    GTGAGCAGCTCTTAACAGCTAGCGAACGTAACTTAGACTTCAGAGATTTATACGATCCTC
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lag of several minutes in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen to plasmin, thus aiding in the localisation of the plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
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                                                                GTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTTTGGTATTATGGACTATAACCT
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of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinses in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clote soon after introduction into the vascular system without significantly activating the circulating blood plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation activation activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
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olytic therapy comprises a streptokinase fused with fibrin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptokinase, SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a chimeric streptkinase-fibrin binding domain (SK-FBD) protein coding sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, a fibrin binding regions of human fibronectin, which are from fibrin binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically
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                                                              1001 Greatricaaarricacearcaarracerreargaretrearacearcearcearriceraaaa
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retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating plasminogen to plasmin, thus aiding in the localisation of the plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising
                                                                                                                                                                                                                                                                                                                                                                      Streptokinase and maltose binding protein fusion protein encoding cDNA.
                     AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG
                                                                                                 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                          TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTACAACAATCTC
                                                                                                                                                                                   GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                                    AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGG
                                                          GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                   GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                         TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAATCTC
                                                                                                                                                               GATGCTTTTGGTATTATGGACTATACCTTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
                                             GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus dysgalactiae subsp. equisimilis.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-terminally deleted streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 45-48; 73pp; English
                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                             AAX80497 standard; cDNA; 2385
                                                                                                                                                                                                                                           CATTTAGCTGGTGGT 1187
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administering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector computating (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving to blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, careful thrombosis, infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence ancomed a streptokinase at least two-fold. The present sequence concerns a streptokinase at least two-fold. The present sequence ancomed and the streptokinase at least two-fold. The present sequence ancomed and the streptokinase at least two-fold. The present sequence and maltose binding protein fusion protein from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2385 BP; 745 A; 547 C; 549 G; 544 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1134; DB 2;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                example of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.6%;
Best Local Similarity 98.7%;
Matches 1143; Conservative
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sequence. The FB fragment has selective affinity for fibrin, low affinity for fibringen, and minimal immunogenicity, imparting thrombus-targetting capability. See also AAQ11649 and AAQ11650
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                                                                                                                                                    Sequence 2030 BP; 673 A; 464 C; 406 G; 487 T; 0 U; 0 Other;
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   thrombus, by linking agent to fibrin binding domain
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                                   Disclosure, Fig 5; 18pp; English
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Matches 1143; Conservative
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fusion protein; ss.
                            2041 GTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCTCTTAACAGCTAGCGAACGT
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/label= streptokinase
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185. .358
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streptokinase;
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                                                                      GTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACA 1047
                                                                                    The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition for dissolving blood clots. Also described are: (1) a modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; anucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
                        ACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAAC
                                     1253 ACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCGGCTCTTAACAGCTAGCGAAC
                                                                                                                       ATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACG
                                                                                                                                            1373 ATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACG
                                                                                                                                                                    ATGACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAATGCTA
                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clof; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus equisimilis native streptokinase encoding cDNA.
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                                                                                                                                                                                                                                                                                                    AAX80492 standard; cDNA; 1242
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                 also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates substrate site for proteolytic cleavage. This reduces the rate of engandation of the streptokinase at least two-fold. The present sequence encodes native streptokinase (nSK). (Updated on 17-OCT-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
thrombosis and arterial thrombosis. The modified streptokinase
                                                                                                                                                                                                                                                                                                                                               Length 1242;
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                                                                                                                                                                                                                                                                                         C; 237 G; 314 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                               Score 1132.6;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                         Sequence 1242 BP; 424 A; 267
                                                                                                                                                                                                                                                                                                                                            73.5%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                       Matches 1141; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibrin binding region;
                                                     GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCGAACGTAAC
                                                                                         TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAATCTC
                                                                                                        TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAATCTC
                                                                                                                                           GATGCTTTTGGTATTATGGACTATACCTTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                           GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                             GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                      GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human Streptococcus equisimilus streptokinase coding sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, fibrin binding regions of human fibronectin, which are from fibrin
Sundaram V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SK; hybrid plasminogen activator; fibri
uman; fibronectin; thrombolytic therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nihalani D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus dysgalactiae subsp. equisimilis.

    S. equisimilis streptokinase coding sequence.

                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptokinase; SK; hybrid plasminogen act
plasminogen; human; fibronectin; thrombol
cardiovascular disorder; fibronectin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "streptokinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1245
/*tag= a
                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                 CATTTAGCTGGTGGT 1187
                                                                                                                                                                                                                                                                        1141 CATTTAGCCTATGAT 1155
                                                                                                                                                                                                                                                                                                                                        AAA37633 standard; DNA; 1245
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            (revised)
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13-OCT-2000
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binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronunced duration, or lag, after exposure of the PA to a suitable comman PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood colots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen to plasmin, thus aiding in the localisation of the plasminogen activation process to the site of pathological thrombus. This covercomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SBP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 1245 BP; 426 A; 267 C; 237 G; 315 T; 0 U; 0 Other;
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Pred. No. 0;
0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           73.5%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 1141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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fusion protein.
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  causing unstable angina, acute myocardial infarction or stroke. The polymucleotide encoding the polypeptide is useful in gene therapy. The vasodilatory action of the protein allower for the use of lower doses of thrombolytic while maintaining the clot dissolving effectiveness of the thrombolytic, and the use of lower doses of the thrombolytic, and the use of lower sequence is the streptokinase cDNA used in the construction of a Maxadilan-Streptokinase fusion protein.
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Pred. No. 0;
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                                                                                                                                                               Maxadilan is a vasodilator peptide
New World sand fly
                                                                                                                                                                                                                                 Sequence 1254 BP; 426 A; 271
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Best Local Similarity 98.8%;
Matches 1141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                           33 ATAGCTGGTCCTGAATGGCTACTAGATCGTCCTTCTGTAAATAACAGCCAATTGGTTGTT
                                                                                                                                                                                                                                                                                                       5935 ATTGCTGGACCTGAGGTGCTTAGACCGTCCATCTGTCAACAACACCACCAATTAGTTGTT
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                       preparation of Maxadilan-Streptokinase fusion protein. It contains maxadilan cDNA, which encodes a vasodilator peptide produced by the salivary gland of the New World sand fly, and streptokinase cDNA
                                                                                                                                                                      73.5%; Score 1132.6; DB 6; Length 8893; 98.8%; Pred. No. 0; ive 0; Mismatches 14; Indels 0;
                                                                                                                        Sequence 8893 BP; 2366 A; 2106 C; 2246 G; 2175 T; 0 U; 0 Other;
                                                                                                                                                                                                Best Local Similarity 98.8
Matches 1141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptokinase, cerebroprotective, cardiant, gene therapy, fusion, vasodilator, thrombolytic, angina, myocardial infarction, stroke, gene therapy, maxadilan, sand fly, plasmid, ds.
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is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                Length 1242;
                                                                 Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;
                                                                                                                             15; Indels
                                                                                            Score 1131; DB 2;
Pred. No. 0;
0; Mismatches 15;
                                                                                              Query Match 73.4%;
Best Local Similarity 98.7%;
Matches 1140; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin; serine protease; fibrin; blood clot; thrombolytic; vaccular thromboembolytic symptom; acute myocardial infarction; fibrinolysis; resistance; ds.
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                                                                                           Length 1242;
  both in acting as a fibrolytic agent and in activating human
                                                Sequence 1242 BP; 421 A; 268 C; 239 G; 314 T; 0 U; 0 Other;
                                                                                         73.2%; Score 1127.8; DB 2; Length 98.5%; Pred. No. 0; ive 0; Mismatches 17; Indels
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                                                                                                                                                                                                                             The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the ProS8-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence encodes mutant SK K59E. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPLg) to plasmin (HPLm), which is a serine protease able to catalyse the sydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thrombombolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus equisimilis H46A, streptokinase; mutant; fibrinolytic; plasma clot; hydrolysis; haemolytic Streptococcus; plasmin, esrine protease; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction; fibrinolysis; resistance; ds.
                                             GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                                   Streptococcus equisimilis mutant streptokinase K59E encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant streptokinase polypeptide - useful as plasmin-resistant thrombolytic agent.
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Synthetic.
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The invention relates to a DNA vector (A) for stable transformation and expression of genes (I) in plastids, where (I) is inserted in an artificial intergene region (ARR) formed by combining two 5-untranslated regions (5-UTRS) of genes that transcribe in different directions and are derived from plants of different divisions or classes. (A) are used to produce transplastomic angiosperms that have improved agronomic properties (e.g. resistance to biotic or abiotic stress) or express a very wide range of agricultural, veterinary, pharmaceutical, nutritional or industrial products, e.g. enzymes, vaccinating antigens, cytokines or immunoglobulins. Use of (A) eliminates the need for a transposon for gene insertion; inserted genes do not require promoters and terminators; and the structure of flanking sequences in (A) ensures universal complicability. Also any selection marker in (A) can be eliminated by homologous recombination. (A) provides efficient and stable expression of genes without causing any functional alterations. This sequence
                                                                                                                                           GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1080
                                                                                                                       GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA vector for transformation and expression in plastids, useful e.g. producing pharmaceutical proteins or improving agronomic properties, gene inserted in artificial intergene region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector; plastid; artificial intergene region; plant;
transplastomic angiosperm; agronomic property; stress resistance;
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                                                                                                                                                                                                                                                                                                               ADM01294 standard; DNA; 7057 BP
                                                                                                                                                                                                              CALTIAGCCIAIGAT 1155
                                                                                                                                                                                          CATTTAGCTGGTGGT 1187
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Sequence 7057 BP; 2029 A; 1543 C; 1608 G; 1877 T; 0 U; 0 Other;

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                                                                                                                           ATTGGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATT
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                                   Gaps
      DB 12; Length 7057;
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                                   28; Indels
                     Pred. No. 2.2e-312;
      Score 1120.2;
                                  0; Mismatches
72.78;
97.68;
                    Best Local Similarity 97.6
Matches 1137; Conservative
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Sequence 1, Appli
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                                                                  January 31, 2006, 16:24:19; Search time 272.069 Seconds (without alignments) 10068.109 Million cell updates/sec
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Sequence 14,
Sequence 39,
Sequence 30,
Sequence 11,
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Sequence 3
Sequence 4
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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3-07-854-5968-46

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5-07-854-596B-27
5-07-854-596B-18
5-07-854-596B-14
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Maximum Match 100%
Listing first 45 summaries
                                               nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                            US-09-940-235-9
1541
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Length 2385;

DB 3;

73.6%; Score 1134;

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2161 CTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGAT 2220
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                                                       1110 GACACCCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGC
                                                                                                                                                                                                                          Sequence 5, Application US/09211542A
Patent No. 6210667
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSE: AROMBERG & SUNSTEIN, LLP
STREET: 125 Summer Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
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Pred. No. 0;
0; Mismatches
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REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)443-9292
                                                                                                      1170 TACCATTTAGCTGGTGGT 1187
                                                                                                                                        2281 TATCATTAGCCTATGAT 2298
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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Best Local Similarity 98.8%;
Matches 1141; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1242 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Massachusetts
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US-09-211-542A-5
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                   15; Indels
Pred. No. 0;
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 Best Local Similarity
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GENERAL INFORMATION:
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              241 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC
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Sequence 1, Application US/08568393B Patent No. 5876999

RESULT 3 US-08-568-393B-1

ORGANISM: Streptococcus equisimilis H46A
INDIVIDUAL ISOLATE: Malke, H., Roe, B., and Ferretti, J. J.;
INDIVIDUAL ISOLATE: "Nucleotide sequence of the streptokinase gene from Streptok
INDIVIDUAL ISOLATE: equisimilis H46A
CELL TYPE: Streptococcus equisimilis H46A ö 152 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC 120 GATCTAACATCACGACCTGCTCATGCAGGAAGACAGGCTTAAGTCCAAAATCA 180 272 181 AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA 240 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC 392 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC 332 241 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC 300 9 1 ATTGCTGGACCTGAGGCTGCTAGACCGTCCACCAACAGCCAATTAGTTGTT AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTGAAATC ATAGCTGGTCCTGAATGGCTACTAGATCGTCCTTCTGTAAATAACAGCCAATTGGTTGTT GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA Gaps ö Length 1242; . streptokinase thrombolytic agents 73.4%; Score 1131; DB 2; Length 1 98.7%; Pred. No. 0; ive 0; Mismatches 15; Indels ADDRESSEE: Jeing & Chang STREET: Two No. 5876999th Second Street, Suite COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB
MEDIUM TYPE: Storage
COMPUTER: Storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MOTGPETfect 6.1 on Window 3.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,393B
FILING DATE: APPLICANT: Hua-Lin Wu
APPLICANT: Guey-Yueh Shi
TITLE OF INVENTION: Preparation of novel
TITLE OF INVENTION: mutants as improved t
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeing & Chang ATTORNEY/AGENT INFORMATION:
NAME: Chi-Ping Chang
REGISTRATION NUMBER: 37,798
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (408) 288-8585
TELEPHONE: (408) 288-8585 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1242 base pairs TYPE: Nucleic Acid STRANDEDNESS: double Conservative CLASSIFICATION: 435 CITY: San Jose STATE: California COUNTRY: USA ZIP: 95113 Similarity HYPOTHETICAL: N ANTI-SENSE: N ORIGINAL SOURCE: TOPOLOGY: 1i Best Local Sımı Matches 1140; US-08-568-393B-1 333 셤 ò

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301 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC 360
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                                                    361 AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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Patent No. 5876999
GENERAL INFORMATION:
APPLICANT: Hua-Lin Wu
APPLICANT: Guey-Yuch Shi
TITLE OF INVENTION: Preparation of novel streptokinase
TITLE OF INVENTION: mutants as improved thrombolytic agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Jeing & Chang
STREET: Two No. 5876999th Second Street, Suite 290
CITY: San Jose
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LOCATION: DNA sequence No. 5876999174 and 175 have been changed LOCATION: from AA to GG, and PROTEIN sequence No. 587699959 has been changed LOCATION: from Lys to Glu.
OTHER INFORMATION:
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                                                                                                                                             MCMEUTER I SECTION OF COMPUTER IN SECTION OF COMPUTER IN SYSTEM: PC-DOS/MS-DOS SOFTWARE: Wordferfect 6.1 on Window 3.1 CURERY APPLICATION DATA:
APPLICATION NUMBER: US/08/568,393B FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chi-Ping Chang REGISTRATION NUMBER: 37,798
REGISTRATION NUMBER: 37,798
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEFAX: (408) 288-855
TELEFAX: (408) 288-855
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1242 base pairs
TYPE: Nucleic Acid
STRANDENNES: double
                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB MEDIUM TYPE: storage
COUNTRY: USA
ZIP: 95113
COMPUTER READABLE FORM:
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                                                            05433/009001
                    NAME: Fraser, Janis K.
REGISTATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEFAM: 617/542-5070
TELEFAM: 200154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2566 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                           34,819
     ATTORNEY/AGENT INFORMATION:
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US-08-488-940-19
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GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
                      GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
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APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STRATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-UUN-1995
CLASSIFICATION: 514
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US-08-488-940-19
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Properties: Streptokinase gene
The gene product binds to human plasminogen
The gene product is an activator of human plasminogen
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                                                                                                                                    Length 1245
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                                                                                                                                                                      Indels
                                                                                                                                  Score 1111.8; DB 2;
Pred. No. 4.1e-310;
0; Mismatches 27;
                 from 1 to 1245 bp mature peptide
 ATCC-9542 strain
                                                                                                                                    Query Match 72.1%;
Best Local Similarity 97.7%;
Matches 1128; Conservative
              FEATURE: from 1 to 12

CTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
 IMMEDIATE SOURCE:
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Sequence 1, Application US/07703778D

Patent No. 5296366

GENERAL INPORMATION:
APPLICANT: Garcia, M.P.E. et al

TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREEFOKINASE, NUCLECTIDE SEQUENCE
TITLE OF INVENTION: OBTAINED, RECOMBINANT DNA AND TRANSFORMED MICROORGANISMS
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Stanger, Michaelson, Spivak and Wallace, Esq.
STREET: P. O. Box 8489

CITT: Red Bank
STATE: New Jersey

COUNTRY: USA
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                 GAAAAGCCGTATGATCCCTTTGATCGCAGTCACCTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                                  GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                        GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
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AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG
                                                                   GAAAAGCCGTATGATCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: MICTOSOFT WORD for Windows
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/07/703,778D
FILING DATE: 19910522
CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: Cent
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)530-6671
TELEFAX: (908)530-6544
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              2035 CATTTAGCCTATGAT 2049
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NAME: Michaelson, Peter L.
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                                                                                                                      GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAGTAGAGGATAATCACGATGAC 1112
                                                                       TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACTAC
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fusion protein"
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CITY: Chicago
STATE: 1L
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Plant Nelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UNN-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPHONE: 310-715-1000
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OTHER INFORMATION: /not OTHER INFORMATION: fusi
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4..1248
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US-07-854-596B-25
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; LOCATION:
US-07-854-596B-25
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                                                                                                          30 ATGATAGCTGGTCCTGAATGGCTACTAGATCGTCCTTCTGTAAATAACAGCCAATTGGTT
                                                                                                                                              4 ATGATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTAGTT
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     Length 1257;
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97.5%; Pred. No. 4.7e-310;
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553

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793 624 853 684 744

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AACGTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACA 1044
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                                                                                                                                                           374 TTGAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGCTGACAAAQATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGAATTTTTGCTAA 673
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  254 ATAAAAGAATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAAT 313
                                                                                                                                                                                                                                              CAAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGCCACATAAACTTGAAAAAGCTG 493
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                                                                                314 TAGTIGITAGCGIIGCIGGIACIGIIGAGGGGACGAAICAAGACAITAGICITAAAITIT
                                                                                                                        TTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTC
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                     CTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAAGATAATCACGAT
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                                                                             GACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAATGCTAGC
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ZIP: 60606
COMPUTER READBLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
APPLICANT: Czaplewski, Lloyd G
APPLICANT: Czaplewski, Tloyd G
APPLICANT: Czaplewski, Lloyd G
APPLICANT: Czaplewski, Lloyd G
APPLICANT: Czaplewski, Tloyd G
CORRESPONDENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
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CURRENT ARE: Facted III.

APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFANS: 312-715-1000
TELEFANS: 312-715-1000
TELEFANS: 312-715-1234
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH 1512 Dase paire
                                                                                                                                                                                                                                                                                                      ; Sequence 27, Application US/07854596B
; Patent No. 5434073
                                                                                                                                                                TACCATTTAGCTGGTGGT 1187
                                                                                                                                                                                                   1144 TATCATTTAGCCTATGAT 1161
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LOCATION: 1..1512
OTHER INFORMATION: /not
OTHER INFORMATION: fuse
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STRANDEDNESS: single
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Best Local Similarity
Matches 1130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicago
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STATE: IL·
COUNTRY: US
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LOCATION:
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; LOCATION:
US-07-854-596B-27
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US-07-854-596B-27
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                                                                                                                                                                                                                                                                                            AUDKESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
STATE: II.
COUNTRY: USA
ZIP: 60606
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRENCE, DOCKET NUMBER: 32,337
TELEFRENCE, DOCKET NUMBER: 312-715-1000
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                                                                                                                              Sequence 18, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION: Each Machael G
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
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streptokinase gene"
                                  1394 CTAGCTATCATTTAGCCTATGAT 1416
                 1165 CTAGCTACCATTTAGCTGGTGGT 1187
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TELEX:
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: 1.1317
OTHER INFORMATION: # Crep
FRATURE:
NAME/KEY: CDS
LOCATION: 4.1308
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LOCATION: 4..1308
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Best Local Similarity
Matches 1126; Conserv
                                                                                                               US-07-854-596B-18
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US-07-854-596B-18
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985 GATGICAACACCAACGAATIGCIAAAAAGCGAGCAGCICITIAACAGCIAGCGAACGIAAC 1044
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Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
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US-07-854-596B-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Streptokinase gene from S.
equisimilis"
                                                                                                                                                                                                                                                                COUNTRY: UGA

21P: 60606
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: MCDONNell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET WUMBER: 26,949
REFERENCE/DOCKET WUMBER: 26,949
RELEFANCE, 1000CKET WUMBER: 312-715-1000
TELLEFAN: 312-715-1234
                                                                       APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Hunter, Michael G
APPLICANT: Graplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. JOhn J. McDonnell
                                                                                                                                                            STREET: Ten South Wacker Drive, Suite 3000 CITY: Chicago
                Sequence 14, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 14.
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
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LOCATION: 1..1335
OTHER INFORMATION: /not
OTHER INFORMATION: equi
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STRANDEDNESS: single
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NAME/KEY:
LOCATION:
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US-07-854-596B-14
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US-07-854-596B-14
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                                       AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEGUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
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US-07-854-596B-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 ATTGCTGGACTGAGGGCTGCTAGACCGTCCATCTGTCAACACAGCCAATTAGTTGTT
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fusion linked by Factor Xa cleavable IEGR"
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Pred. No. 3.7e-309;
0; Mismatches 29; Indels
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCES. 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION 1NPERMATION:
NAME: MCDORNELL, JOHN J
REGISTRATION NUMBER: 26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
71.9%;
Best Local Similarity 97.5%;
Matches 1126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1458
OTHER INFORMATION: fusion
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 312-715-1234
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FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1449
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US-07-854-596B-42
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                                                      GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGCTCTCAAA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
ITILE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSE: Dr. John J. McDonnell
STREFT: Ten South Wacker Drive, Suite 3000
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Pred. No. 3.7e-309;
0; Mismatches 29; Indels
                                     COMPUTER: PORDAGE
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CORRENT APPLICATION NUMBER: US/07/854,596B
FILING BATE: 03-UUN-1992
CLASSIFICATION NUMBER: 26,949
REGISTRATION NUMBER: 312-715-1000
TELEFAX: 312-715-1134
TELEFAX: 312-715-1000
TELEFAX: 312-715
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Best Local Similarity 97.5%;
Matches 1126; Conservative (
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LOCATION: 1..1467
OTHER INFORMATION: /note
OTHER INFORMATION: fusio.
FRATURE:
NAME/KEY: CDS
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; LOCATION:
US-07-854-596B-46
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FEATURE:
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              573 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
                                    GCTCAAGCACAAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
                                                                                                                     667 GCTCAAGCACAAAGCATTTTAAACAAAACCCATCCAGGCTATACGATTTATGAACGTGAC
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APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Menendez, Alina Seralena
APPLICANT: Menendez, Alina Seralena
APPLICANT: Bscalona, Elder Pupo
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILE REPERROCE: Sequence Listings 1-14 re: 976-5
Patent No. 6309873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.4%; Score 1084.4; DB 3; Best Local Similarity 98.1%; Pred. No. 3.2e-302; Matches 1097; Conservative 0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/374,038 CURRENT FILING DATE: 1999-08-13 NUMBER OF SEQ ID NOS: 14 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Streptococcus equisimilis US-09-374-038-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 11, Application US/09374038; Patent No. 6309873; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..2589
OTHER INPORMATION: /note=
OTHER *INFORMATION: "OmpAL-Streptokinase-streptokinase fusion linked
OTHER INFORMATION: by thrombin-cleavable VELQGVVPRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 AAACCATTTGCTACTGATAGTGGCGCGATGCCACATAAAACTTGAAAAAGCTGACTTACTA
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71.9%; Score 1108.6; DB 2; Length 2589;
Best Local Similarity 97.5%; Pred. No. 4.7e-309;
Matches 1126; Conservative 0; Mismatches 29; Indels 0;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1034
                                                                                                                                                                                                                                  TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: .mat_peptide
; LOCATION: 4..2580
US-07-854-596B-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 4..2580
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NAME/KEY: CDS
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Qy         1150         CCGAAGGAGAATGCTAGCTACCATTTAGCTGGT         1187	ESULT 15 S-09-658-179-1 Sequence 11, Patent No. 64 GENERAL INFOK APPLICANT:	; APPLICANT: Ojalvo, Ariana García ; APPLICANT: Menendez, Alina Seralena ; APPLICANT: Escalona, Elder Pupo ; APPLICANT: Masso, Julio Raul Fernandez ; APPLICANT: Griego, Martha De Jesus Gonzalez ; TITLE OF INVENTION: STREPTOKINAS	Δ, (	; LENGTH: 1209 ; TYPE: DNA ; ORGANISM: Streptococcus equisimilis US-09-658-179-11	Query Match 70.4%; Score 1084.4; DB 3; Length 1209; Best Local Similarity 98.1%; Pred. No. 3.2e-302; Matches 1097; Conservative 0; Mismatches 21; Indels 0; Gaps 0;	Oy 70 TAAATAACAGCCAATTGGTTGTTAGCGTTGCTGGTACTGTTGAGGGACGAACGA	130 TTAGTCTTAAATTTTTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAGACAG [	190 AGCAAGGCTTAAGTCCAAAATCAATTGCTACTGATAGTGGCGCGATGTCACATA	dy 250 AACTTGAGAAGCTGACTTACTAAGGACTATTCAAGAACAATTGATCGCTAACGTCCACA 309	Db 242 GTAACGACGACTACTTGAGGTCATTGATTTTGCAAGCGATGCATTACTGATACTACTGATGAA 301  Qy 370 ACGGCAAGGTCTTGCTGACAAGGTTCGGTAACCTTGCCGACCGA	362 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	Oy 490 ACCAAGGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATG 549	Oy 550 ACGATITCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACA 609	Oy 610 CCATCACATCTCAGAATTACTAGCTCAAGCACAAAGCATTTAAACAAAAACCACCAG 669
70 TAANTAACAGCCAATTGGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACA 129 	130 TTAGTCTTAAATTTTTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAGACGG 189	250 AACTIGAGAAAGCIGACTTACTAAAGGCTATICAAGAACAATIGAICGCIAACGICCACA 309	GTAACGACGACTACTITGAGGTCAITGAITTTGCAAGCGATGCAACCATTACTGATCGAA 30 ACGGCAAGGTCTACTTTGCTGACAAGATGGTTCGGTAACCTTGCCGACCAACGTTGCTGACGACGAAGATGTTCGGTAACCTTGCCGACCCAACCTGTCC 42	aagaattititgctaagggacatgtgggggttagaccatataaagaaaaaccaatacaa 	490 ACCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATG 549 422 ALCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATG 549 422 ATCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATG 481 550 ACGATTTCACACCCAGATCTCAAAGATATAAAGCTAATAGAAAAAAAA	ACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCAGCCACCAGCCACAAACAA		602 GCTATACGATTTATGAACGTGACTCCTCAATCGTCATGACAATGACATTTTCCGTA 661 730 CGATTTTACCAATGATTAACATTACTTACCGTGAAAAATCGGGAACAATGATA 789	662 CGATTTTACCAATGGATCAAGAGTTTACTTACCATGTCAAAAATCGGGAACAAGCTTATG 721 790 GGATCAATAAAAAATCTGGTCTGAATGAAGAAAAAACAACACTGACTG	722 AGAICAAIAAAAAAICTGGTCTGAATGAAGAAATAAACAACAGTGACCTGATCTCTGAGA 781 850 AAVATTACGTCCTTAAAAAGGGGAAAAGCCGTATGATCGCTTTGATCGCAGTCACTTGA 909 11	aactottcaccatcaaatacgttgatgtcgataccaacgaattgctaaaagtgagcagc 		1090 AACTAGGATAACATGACGATGGTTTTGGTATTATGGACTATACCTTAACTGGAA 1089 1090 AACTAGGATACTGTACAACAATGTGGATGCTTTTGGTATTATGGACTATACCTTAACTGGAA 1021 1090 AACTAGGAGATAACGATGACGATGACTATTAGGACTATAACGGAGAA 1021	

	2 ccgaagaagaargcraactarcartragccratgar 1119	b 1082	đ
	0 CCGAAGGAGAGAATGCTACCATTTAGCTGGTGGT 1187	y 1150	ò
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6	0 AAGTAGAGGATAATCACGATGACACCAACCGTATCATAACCGTTTATATGGGCAAGCGAC 1149	у 1090	δ
п	2 CTAAACTACTCTACAACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAA 1021	b 962	q
6	0 CTAÂACTACTACAACAACTCTGGATGCTTTTTGGTATTATGGACTATACTGGAA 1089	y 1030	Š
	2 TCTTAACAGCTAGCGAACGTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGG 961	b 902	ф
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	2 AACTGTTCACCATCAAATACGTTGATGTCAACGCAACGAATTGCTAAAAAGCGAGCAGC 901	b 842	đ
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	0 CGATTTTACCAATGGATCAAGAGTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATA 789	у 730	õ
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	0 GCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACATTTTCCGTA 729	у 670	ਠੇ

Search completed: February 1, 2006, 12:43:41 Job time : 273.069 secs Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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Sequence 1, Appli
Sequence 657, App
Sequence 3, Appli
Sequence 49, Appli
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10008.068 Million cell updates/sec
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4288, Ap
49, Appl
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Sequence 5, Appli
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Sequence 10,
                                                                                             January 31, 2006, 17:06:30 ; Search time 1273.28 Seconds
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GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
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US-10-956-157-4995
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Maximum Match 100%
Listing first 45 summaries
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Sequence 3	Sequence 5	Sequence 6	Sequence 6	Sequence 7	Sequence 7	Sequence 1	Sequence 2	Sequence 7	Sequence 6	Sequence 6	Sequence 8	Sequence 6	Sequence 5	Sequence 6	Sequence 5	Sequence 2	Sequence 7		Sequence 7	Sequence 2	Sequence 6
US-10-831-704-38	US-09-964-824A-574	US-10-171-311-63	US-10-236-031B-69	US-10-374-979-75	US-10-182-936A-75	US-10-641-643-1289	US-10-717-597-222	US-10-788-792-79	US-10-477-238A-654	US-10-680-287A-654	US-10-278-698-88	US-10-278-698-603	US-10-843-641A-5877	US-10-477-173-654	US-10-852-335A-52	US-10-084-817-2	US-10-741-601-77	US-10-741-600-245	US-10-741-601-78	US-10-741-600-246	US-10-098-841-6
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24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram
APPLIC
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                                 Sequence 9, Application US/09940235; Publication No. US20030059921A1; GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
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ORGANISM: Artificial Sequence
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Matches 1541; Conser
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US-09-940-235-9
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APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Ray, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Shajagopal, Kammara
APPLICANT: Sundaram, Vasudha
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: US/09/040,235
TITLE OF INVENTION: US/09/04-09
TITLE OF INVENTION WUMBER: US/09/940,235
CURRENT APPLICATION NUMBER: 09/411,349
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 113 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
TENNETH: 1327
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Pred. No. 0;
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Best Local Similarity 99.6%;
Matches 1182; Conservative
Kumar, Rajesh
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Sequence 6, Application US/09940235 Publication No. US20030059921A1 GENERAL INFORMATION:

Qy         1 TTTGTTTAACTTTAAGAAGAGATATACCATGATAGCTGGTCCTGAATGGCTACTAGATC         60           Db         101 TTTGTTTAACTTTTAAGAAGAAGAATATACCATGATTGCTGGACTGAGTGGCTGCTAGACC         160		QY 121 ATCAAGACATTAGTCTTAAATTTTTTGAAATCGATCTAACATCACGACCTGCTCATGGAG 180	OY 181 GAAAGACGGAGGCTTAAGTCCAAAATCAAAACCATTTGCTACTGATAGTGGGGGGG 240	OY 241 TGTCACATAAACTTGAGAAAGCTGACTTACTAAAGGCTATTCAAGAACAATTGATCGCTA 300	OY 301 ACGTCCACAGTAACGACGACTACTTTGAGTCATTGATTTTGCAAGCGATGCAACCATTA 360	Qy 361 CTGATCGAAACGCCAAGGTCTACTTTGCTGACAAAAGATCGGTCACCTTGCCGACCC 420	Qy         421 AACCTGTCGAAGAATTTTTGGTAAGGGGACATGGGGGGTTAGACCATATAAAGAAAAC 480           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 481 CAATACAAACCAAGGGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAA 540	QY 541 ACCCTGATGACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTA 600	QY 601 TCGGTGACACCATCACAAGAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAA 660 	QY 661 ACCACCCAGGCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACA 720	Qy 721 TTTTCCGTACGATTTTACCAATGGATCAAGAGTTTACTTAC	Qy 781 AAGCTTAIAGGATCAATAAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGA 840	Oy 841 TCTCTGAGAAATATTACGTCCTTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCA 900	Qy 901 GTCACTTGAAACTGTTCACCATCAAATACGTTGATGTCGATACCAACGAATTGCTAAAAA 960 1001 GTCACTTGAAACTGTTCACCATCAAATACGTTGATGTCGATACCAACGAATTGCTAAAAA 1060	Qy 961 GTGAGCAGCTCTTAACAGCGAACGTAACTTAGACTTCAGAGATTTATACGATCCTC 1020	1021 GTGATAAGGCTAAACTACTCCAACAATGCTTTTTGGTATTATGGACTATACCT	Db 1121 GTGATAAGGCTAAACTACTGTACAACAATCTCGATGCTTTTGGTATTATGGACTATAACCT 1180
661 ACCACCAGGCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACA 72	ATGACA 77 3GGAAC 78 [[[[]]	71 IIIICCGIACGAITITACCAATGGAICAGGGITTACTGACGGIGITAAAAATC 781 AAGCTTATAGGATCAATAAAAATCTGGTCTGAATGAAGAAATAAACACCCTC 831 AACCTTATAGGATCAATAAAAAATAACCTTC	841 TCTCTGAGAAATATTACGTCCTTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCA 90 841 TCTCTGAGAAATATTACGTCCTTAAAAAAGGGGAAAAGCCGTATGATCGCTTTGATCGCA 90 891 TCTCTGAGAAATATTACGTCCTTAAAAAAAGCGCAAAAGCCCTATTGATCGCA 90	901 GTCACTTGAACTGTTCACCATCAATACGTTGATGCCCTATGATCCCTTGATCGCTAGAAAA 9 901 GTCACTTGAACTGTTCACCATCAAAAAA 9 911 GTCACTTGAACTGTTCACCATCAATACGTTGATGCCATCAACAA 9 912 GTCACTTGAAAATCCTATCAATACCTTTCAACTAACCAACC	961 GTGAGGAGCTCTTAACAGCTAGCGAACGTAAGTTAGAGCTTCAGAGATTTATACAGCTAGCGAACGTAACCTTAGAGCTTTAGAGTTTATAACCTAAGAGAACTTAGAGCTTAGAGATTTATAACAGAAACTAAGAGAAAAAAAA	1021 GTGATAAGGCTAAACTACTACAACATCTCGATGCTTTTGGTATTATGGACTATACCT 1 1071 GTGATAAGGCTAAACTACTCTACAATCTCGATGCTTTTTGGTATTATGGACTATACCT 1 1071 GTGATAAGGCTAAACTACTACAATCTCGATGCTTTTTGGTATTATGGACTAATCTCAAACTTCGAATCTCGATAAGGCTAAACTACTAAACTACTCGAAACTTCGAATCTCGATAAGGCTAAACTAAACTACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAAACTAAAAAA	TAACTGGAAAAGTAGGGATAATCACGATGACCCAACCGTATCATAACGTTTATATGG	1191 IAACIGGAAAAAGAAAAATCACAATGACAACCAATCAACCGTTAATGG 119 1141 GCAAGCGACCCGAAGGAGAGAATGCTAGCTACCATTTAGCTGGTGGT 1187 1191 GCAAGCGACCGAACGCAAAGCTAACTAGCTACCATTTAGCTGGTGGT 1187 1191 GCAAGCCAACCCAAACCAAACCTAACTAATAGCTAAAACAAAAACAAAAAAAA		Sequence 5, Application No. US, GENERAL INFORMATION NO. US, Application No. US, Applic	APPLICANT: APPLICANT: APPLICANT:	APPLICANT: Nimidaram, APPLICANT: Yadav, Ma TITLE OF INVENTION: N	TITLE OF INVENTION: FROIBLES POSSESSING TITLE OF INVENTION: CHARACTERISTICS AND TITLE OF INVENTION: PROTEIN FILE REFERENCE: 07064-009002	; CURRENT APPLICATION NUMBER: US/09/940,235; CURRENT FILING DATE: 2002-04-09; PRIOR APPLICATION NUMBER: 09/471,349; PRIOR FILING DATE: 1999-12-23		; SEQ 1D NO 5 ; LEGETH: 1377 ; TYPE: DNA ; ORGANISM: Streptococcus equisimilis	940-235-5 75.7%; Scc	Similarity 98.9%;

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APPLICANT: Kunar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Sundaram, Vasudha
APPLICANT: STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION OF SAID
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     GTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
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PRIOR APPLICATION NUMBER: 09/471,349
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APPLICANT: Roy, Chait
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahahir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 0764-009000;
CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1782
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0; Mismatches
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Publication No. US20030059921A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 1142; Conservative
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APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
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Best Local Similarity
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                                          TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTTCTACAACAATCTC
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; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Nickbarg, Blliot
; APPLICANT: Minter, Lourie
; APPLICANT: Minter, Lourie
; TITLE OF INVENTION: SURRACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: Patentin version 3.0
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; ORGANISM: Streptococcus pyogenes
US-10-474-792-657
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Best Local Similarity 91.3
Matches 1054; Conservative
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98.8%; Pred. No. 0;
ive 0; Mismatches
                      3825/DEL/98
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOPTWARE: PastSEQ for Windows Version
SEQ ID NO 1
                                                                                                  TYPE: DNA
ORGANISM: Streptococcus equisimilis
                                                                                                                                                                                                             Best Local Similarity 98.8
Matches 1141; Conservative
                                                                                                                                                       ; LOCATION: (1)...(1242)
US-09-940-235-1
                                                                                                                                            NAME/KEY: CDS
                                                                                        LENGTH: 1245
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Query Match
Best Local Similarity 100.
Matches 330; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                         ; LOCATION: (1)...(777)
US-09-940-235-3
                                                                                                                                                                                                                            NAME/KEY: CDS
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379 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC 438
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Publication No. US20030059921A1
GENERAL INFORMATION:
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
                                                                                                 619 GATACTAAGCTATTGAAAAACACTATCGGTGACACCATCACACTCTCAAGAATTACTA
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; Sequence 49, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnalyan, Arul M.
; APPLICANT: Chinnalyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun M.
; TITLE OF INVERTION: Expression Profile of Prostate Cancer:
; TILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT PILING DATE: 2002-08-01
; PRIOR PILING DATE: 2001-08-02
; PRIOR PILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Version 3.2
; SEQ ID NO 49
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100.0%; Pred. No. 7.2e-84;
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TITLE OF INVENTION: CHARACTERISTICS AND A P. TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: 09/471,349
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR PILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO: 280 ID NOS: 28
LENGTH: 777
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1449 ACAGGCAACGGCCGAGGAGGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 1508
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Sequence 70, Application US/10741601

Sequence 70, Application US/10741601

Sequence 70, Application US/10741601

GENERAL INFORMATION:

TITLE OF INVENTION: STENCELL, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: STENCELS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1500

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 70
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100.0%; Pred. No. 1.3e-83;
tive 0; Mismatches 0;
      1509 AGCGGATCTGGCCCCTTCACCGATGTTCGT 1538
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                                                                                                                                 FULLICANT: APPLICATION US/1090935
FUBLICATION NO. US20050136493A1
GENERAL INFORMATION:
APPLICANT: Rubin, Mark A.
APPLICANT: Chinnalyan, Arul M.
APPLICANT: Laxman, Bharathi
APPLICANT: Laxman, Bharathi
FILE REFERENCE: UM-09098
CURRENT APPLICATION: AMACR Cancer
CURRENT APPLICATION NUMBER: US/10/909,035
CURRENT APPLICATION NUMBER: US/10/909,035
CURRENT FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PATENTIN VERSION 3.2
                            897 AGGGGATCTGGCCCCTTCACCGATGTTCGT
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Matches 330; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-741-601-70
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US-10-909-035-49
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LENGTH: 2127
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Publication No. US20050118625A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WILLIAM
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATON NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEC ID NOS: 319805
SOFTWARE: Patentin version 3.2
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                                                                             1209 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCGGACTTCCTATGTGGGTCGGAGAAACG 1268
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      Length 2127;
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21.4%; Score 330; DB 6; I
100.0%; Pred. No. 1.3e-83;
tive 0; Mismatches 0;
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Query Match
Best Local Similarity 100.
Matches 330; Conservative
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Best Local Similarity 100.
Matches 330; Conservative
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US-10-956-157-4288
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US-10-956-157-4288
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LENGTH: 2127
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE PERERECE; CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 238
LENGTH: 2443
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                                                                                      1209 CCCATAGCTGAGAAGTGTTTTGATCATGCTGGGACTTCCTATGTGTGGTCGGAGAAACG 1268
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                 Length 2443;
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                                                 Indels
             21.4%; Score 330; DB 7; I
100.0%; Pred. No. 1.4e-83;
Live 0; Mismatches 0;
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Sequence 238, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
           Query Match
Best Local Similarity 100.
Matches 330; Conservative
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; ORGANISM: Homo sapiens
US-10-741-600-238
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                                                                                                                                                                          US-10-741-601-75

Sequence 75, Application US/10741601

Sequence 75, Application US/10741601

Publication No. USZO040166519A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REPREBUCE: CLOO1500

CURRENT PILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE: PastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.4e-83;
Matches 330; Conservative 0; Mismatches 0;
                                1213 AGCGGATCTGGCCCCTTCACCGATGTTCGT 1242
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1509 AGCGGATCTGGCCCCTTCACCGATGTTCGT
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; ORGANISM: Homo sapiens
US-10-741-601-75
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Maximum DB
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Maximum Match 10
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Perfect score:
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: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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Million cell updates/sec
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Sequence 9, Appli
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Sequence 117, App
Sequence 111, App
Sequence 111, App
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Sequence 114, App
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Sequence 116, App
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Sequence 117, App
Sequence 118, App
Sequence 119, App
Sequence 110, App
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2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.4	2.5	2.5	2.5	2.5	2.7	3.4	3.4	3.4	3.4	3.6	10.4	14.7
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US-10-995-561-13497	US-10-750-623-35934	US-10-750-185-35934	US-10-995-561-13314	US-10-995-561-53161	US-10-240-708-27	US-11-136-527-227	US-11-136-527-4323	US-10-995-561-53153	US-10-995-561-52927	US-10-775-169-193	US-11-121-086-13	US-10-631-558-16	US-10-995-561-115	US-10-631-558-19	US-11-074-176-131	US-10-631-558-18	US-10-631-558-7	US-10-631-558-14	US-10-631-558-13	US-10-995-561-26955	US-10-995-561-13237	US-11-136-527-2446
Sequence 13497, A	Sequence 35934, A	Sequence 35934, A	Sequence 13314, A	5316	Sequence 27, Appl	227,	Sequence 4323, Ap		52927	193,	13,	Sequence 16, Appl	Sequence 115, App	Sequence 19, Appl	Sequence 131, App	Sequence 18, Appl	Sequence 7, Appli	Sequence 14, Appl	Sequence 13, Appl	Sequence 26955, A	Sequence 13237, A	Sequence 2446, Ap

## ALIGNMENTS

RESULT 1 US-10-631-558-9

; Sequence 9, Application US/10631558 ; Publication No. US20050260598A1

GENERAL INFORMATION:

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APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Roy, Chait
APPLICANT: Roy, Chait
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Nihalani, Deepak
APPLICANT: Nobavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION UNMBER: US/10/631,558
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: US/09/940,235
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                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1541; Conservative 0
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SEQ ID NO 9
LENGTH: 1541
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Hybrid cassette
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
61 GTCCTTCTGTAAATAACAGCCAATTGGTTGGTTTAGCGTTGCTGGTACTGTTGAGGGGACGA 120
                                                                                                                                     μ
                                                                                                             TTTGTTTAACTTTAAGAAGGAGATATACCATGATAGCTGGTCCTGAATGGCTACTAGATC
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Pred. No. 0;
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Qy         1201 AGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGGGACTTCCTATGTGGTG         1201           Db         1201 AGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGGGACTTCCTATGTGGTG         1201           CadaaACGTGGAAGTCTACAAGATTGATCATGCTGGAACTTGCTTG	RESULT 2  (Sequence 12, Application US/10631558  (Sequence 12, Application US/10631558  (Sequence 12, Application US/10631558  (Sequence 12, Application No. 120005260598A1  (Sequence 12, Application No. 120005260598A1  (Sequence 12, Application No. 12000526059BA1  (Septicary: School Coling No. Chair Sequence Septicary: School Coling No. Chair Septicary: School Chair Septicary:	
61 GTCCTTCTGTAAATAACAGCCAATTGGTTGTTGCGTTGC	481 CARTACARACCAGGGARATCTGTTGATGTGGARTATCTGTACAGTTTACTCCCTTAA 540 481 CARTACARACCAGGGARATCTGTTGATGTGGARTATCTGTACAGTTTACTCCCTTAA 540 481 CARTACARACCAGGGACCAGGTCTCARACATTGACACACTTCACCCTTAA 540 541 ACCCTGATGACGATTTCAGACCAGGTCTCARACATTCACACACACACACACACACACACACACAC	

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                                 CATTTAGCTGGTGGTGGCCAGGCGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGAT
                                                                                                    GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
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Sequence 10. Application US/10631558

Publication No. US20050260598A1

GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Rajespal, Kammara
APPLICANT: Rajespal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 19471,349
PRIOR FILING DATE: 1999-12-23
PRIOR RILING DATE: 1999-12-23
PRIOR RILING DATE: 1999-12-24
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
SEQ ID NO 10
LENGTH: 1661
TYPE: DNA
DESCRIPTION APPLICATION WINDOWS Version 4.0
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Best Local Similarity 98.8%;
Matches 1194; Conservative
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Hybrid cassette
                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial FEATURE:
                     121
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ATCAAGACATTAGTCTTAAATTTTTTGAAATCGATCTAACATCACGACCTGCTCATGGAG
                                                                           GTCCTTCTGTAAATAACAGCCAATTGGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGA 120
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                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                               Score 1185;
Pred. No. 0;
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APPLICANT: Sabni, Girish
APPLICANT: Sabni, Girish
APPLICANT: Sabni, Girish
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: UNMERR: US/10/631,558
CURRENT APPLICATION NUMBER: US/09/940,235
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOCTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 6
TENGTH: 11777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1179; DE
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Streptococcus equisimilis US-10-631-558-6
                                 ; Sequence 6, Application US/10631558; Publication No. US20050260598A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.5%;
Best Local Similarity 99.6%;
Matches 1182; Conservative
                                                                                   APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Nihalani, Gespak
APPLICANT: Nihalani, Gespak
APPLICANT: Nihalani, Gespak
APPLICANT: Nihalani, Gespak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
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TITLE OF INVENTION PROTEINS
TITLE OF INVENTION NUMBER: US/10/631,558
CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US/99/40,235
PRIOR FILING DATE: 1999-12-23
PRIOR PLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER: OR SECTION NUMBER: IN 3825/DEL/98
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US-10-631-558-5
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                                                         ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC 392
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APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
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                                  GTGAGCAGCTCTTAACAGCTAGCGAACGTAACTTAGACTTCAGAGATTTATACGATCCTC
                                                                     GTGATAAGGCTAAAACTACTACAACAATCTCGATGCTTTTGGTATTATGGACTATAACCT
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Pred. No. 0;
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Similarity 98.9%;
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Best Local Similarity 98.9
Matches 1142; Conservative
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; LOCATION: (1)...(1242)
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APPLICANT: Rajagopal, Kammara

APPLICANT: Nihalani, Deepak

APPLICANT: Nihalani, Deepak

APPLICANT: Nihalani, Deepak

APPLICANT: Nihalani, Deepak

APPLICANT: Noutern, Vasudha

APPLICANT: Yadav, Mahavir

TITLE OF INVENTION: NOUTER CLOT-SPECIFIC STREPTOKINASE

TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SI

TITLE OF INVENTION: PROTEIN

TITLE OF INVENTION NUMBER: US/10/631,558

CURRENT APPLICATION NUMBER: US/09/940,235

PRIOR APPLICATION NUMBER: 09/471,349

PRIOR APPLICATION NUMBER: 09/471,349

PRIOR APPLICATION NUMBER: 1999-12-23

PRIOR APPLICATION NUMBER: 1999-12-23

PRIOR APPLICATION NUMBER: 1998-12-24

NUMBER OF SEQ ID NOS: 28

CONTMERS FOR THE PREPARATION OF SEQ ID NOS: 28

CONTMERS FOR SECEN OF WINDOWS TO THE PREPARATION OF SEQ ID NOS: 28
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Pred. No. 0;
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US-10-631-558-3
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LENGTH: 777
TYPE: DNA
ORGANISM: Homo
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PEATURE:

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CURRENT APPLICATION NUMBER: US/10/631,558; CURRENT FILING DATE: 2003-07-31; PRIOR APPLICATION NUMBER: US/09/940,235; PRIOR FILING DATE: 2002-04-09; PRIOR PRIOR DATE: 1999-12-23; PRIOR APPLICATION NUMBER: US/04/11,349; PRIOR PILING DATE: 1999-12-23; PRIOR APPLICATION NUMBER: IN 3825/DEL/98; PRIOR PILING DATE: 1998-12-24; NUMBER: OF SEQ ID NOS: 28; SOPTWARE: PASTSEQ for Windows Version 4.0; SEQ ID NO 3; LENGTH: 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10631558
Publication No. US20050260598A1
                                                                                                                                                                                                                                                                                                            APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF THE REFERENCE: 07644-009002
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICAT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
PILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20050272054A1
GENERAL INFORMATION
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0
Matches 330; Conservative
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ORGANISM: Homo sapiens
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US-10-995-561-105
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US-10-995-561-112
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT PILING NOMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
                                                                                                                                                                                                              508 TGGGAGAAGCCCTACCAAGGCTGGATGATGTAGTACTTGCCTGGGAGAAGGCAGC
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100.0%; Pred. No. 9.1e-95;
Live 0; Mismatches 0;
                                                                                          Score 330; DB 7; 1
Pred. No. 4.4e-95;
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                                                                         21.4%; Sco. No. 100.0%; Pred. No. 0; Mismatches
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                                                                                     Query Match
Best Local Similarity 100.
Matches 330; Conservative
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; ORGANISM: Homo sapiens
US-10-995-561-114
  ; NAME/KEY: CDS
; LOCATION: (1)...(777)
US-10-631-558-3
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NAME/KEY: CDS
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US-10-995-561-117

Sequence 117, Application US/10995561

Sequence 117, Application US/1099561

Publication No.; US20050272054A1

APPLICANT: CARGILL, Michele et al.

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: CENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOCTWARE: FRASTSEQ for Windows Version 4.0

SEQ ID NO 117

LENGTH: 7823
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-112
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Best Local Similarity
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ORGANISM: Homo sapiens
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                   AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                                                        GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT
                                                                                                                                                           TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTTGGGAGAAGGCAGC
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AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                                    GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT
                                                                                                                                       TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC
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100.0%; Pred. No. 1.9e-94;
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; Pred. No. 1.7e-94;
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Sequence 113, Application US/10995561 Publication No. US20050272054A1 GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOPTWARE: PastSEQ for Windows Version 4.0

RESPONSE,

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Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
ITILE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
ITILE OF INVENTION: GENETIC POLYMORPHISMS AND DRUG RESPON
ITILE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEG ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 111
LENGTH: 7848
TYPE: DNA
ORGANISM: Homo sapiens
RESULT 14
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US-10-995-561-111
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| Publication No. US20050272054A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al.
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
| TITLE OF INVENTION: DETECTION AND USES THEREOF
| TITLE OF INVENTION: DETECTION AND USES THEREOF
| TITLE OF INVENTION: DETECTION AND USES THEREOF
| TITLE OF INVENTION: DATE: 2004-11-24
| CURRENT APPLICATION NUMBER: US/10/995,561
| CURRENT FILING DATE: 2004-11-24
| NUMBER OF SEQ ID NOS: 85702
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 108
| LENGTH: 7959
| TYPE: DNA ORGANISM: Homo sapiens
| US-10-995-561-108 |
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                                                                                                                                Query Match 21.4%; Score 330; DB 7; I
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 330; Conservative 0; Mismatches 0;
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                                          TYPE: DNA
CORGANISM: Homo sapiens
US-10-995-561-113
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US-10-995-561-108
SEQ ID NO 113
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Db 1093 AGAATTGGAGACACGTGGAAGATATCGAGGAAACCTGCTCCAGTGCATCTGC 1152

Qy 1449 ACAGGCAACGCCGAGGAGAGTGGAAGTGTGAGGACCTCTGTGCAGACCATCG 1508

Db 1153 ACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGGCACCTCTGTGCAGACCACTCG 1212

Qy 1509 AGCGGATCTGGCCCTTCACCGATGTTCGT 1538

Db 1213 AGCGGATCTGCCCTTCACCGATGTTCGT 1242

Search completed: February 1, 2006, 14:43:12

Sob time : 285.911 secs
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Result
No.
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Maximum DB
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Perfect score:
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Score
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seq length: 2000000000
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                                                                                                                                                                                                               Match Length
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11385.988 Million cell updates/sec
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1541
Listing first 45 summaries
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gb_est5:*
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AI743013
BF956982
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CR749281
HSM806992
AI095589
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BC100030
CR749316
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AU140993
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CN482442
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CN419611 170005313
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BC100030
CR749316
BX640608
CR749281
BX640875
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AU140993
BM715855
AU140971
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5 UI-E-EJO-
L AU140971
         Homo sapi
56022208J
56022208H
wg85a12.x
QV4-NN114
PM4-BN017
                                                             Homo sapi
BX391752
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249.4	251.8	256.8	261.8	264	268	268.6	271.8	274	277.8	280	281	287	287	296.4	297.4	298	304	305	307	310	315.4	317
16.2	16.3	16.7	17.0	17.1	17.4	17.4	17.6	17.8	18.0	18.2	18.2	18.6	18.6	19.2	19.3	19.3	19.7	19.8	19.9	20.1	20.5	20.6
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BX327266 BX327266	CN419631 170005321	DN123922 1124284 M	CB536952 772021 MA	W46530 zc32h07.rl	BQ574857 UI-H-EZ1-	BI058354 PM3-GN051		BF956977 QV4-NN114	BQ292415 PM0-AN008	BG900107 HOA51-1-C	CN419657 170004553	CN419649 170005315	CN419650 170005315	AA852090 NHTBCael0	BG945197 PM0-AN008	AL603599 DKFZp686K		AI093548 qb08h09.x	AA492032 ng55a12.s	CN419658 170005315	AL706215 DKFZp686J	AU140789 AU140789

## ALIGNMENTS

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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SOURCE
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VERSION
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AL603368
LOCUS
ORIGIN
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                                                                                                                                                                                                           source
                                                                                                                                                                                                                                              No s1 sequence available.
This clone (DKFZp686C067) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 451)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemunpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKFZp686C067_r1 686 (synonym: h
DKFZp686C067_5', mRNA sequence.
AL603368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MIPS
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dominidae;
                                                                            /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686C067"
/dev_stage="adult"
/lab_host="DH10B"
                 /clone_lib="686 (synonym:
/note="Vector: pTriplEx2;
cDNA-collection"
                                                                                                                                                                                                                            Location/Qualifiers
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                                hlcc3)"
Site_1:
                                  SfiIA; Site_2: SfiIB;
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Query Match Best Local Similarity

21.4%;

Score 330; DB 1; Pred. No. 1.1e-82;

Length 451;

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Incrementary human pericytes in culture. A directionally cloned primary human pericytes in culture. A directionally cloned cDNA library in the pSPORTI vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGCCC(T)15-3']. cDNA was
                                                                                                                                                                                                 GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT 1388
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hw20d08.y1 Human primary human ocular pericytes. Unamplified (hw)
Homo sapiens cDNA clone hw20d08 5', mRNA sequence.
                                                                                                                           269 TGGGAGAAGCCCTACCAACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGAGGCAGC 328
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 621)
Tsai,J.Y. and Wistow,G.
Expressed sequence tag analysis of cultured primary human ocular
                              209 CCCATAGCTGAGAAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAAAACG
                                                                                                    TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC
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Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
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Plate: 20 row: d column: 08
Seq primer: MISRP1 reverse primer
Location/Qualifiers
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/dev_stage="Adult"
/lab_host="EMDH10B"
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/clone="hw20d08"
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Unpublished (2004)
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1 (bases 1 to 560)

Bandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.

Transcriptome characterization elucidates signaling networks that
Control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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T7000531856084 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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CN419585.1 GI:47407179
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Geron Corporation
33 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 560 Std Error: 0.00.
Location/Qualifiers
  Indels
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  0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 330; Conservative
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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S.,
Lebkowski, J and Stanton, L.W.
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CN419611.1 GI:47407205
EST.
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Regenerative Medicine
                                                                                                                                                                                                                        Email: rbrandenberger@geron.com
Insert Length: 626 Std Error: 0.00.
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1 (bases 1 to 626)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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650 473 7760
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/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived_from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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                                                                                                                                                   organism="Homo sapiens"
/mol_type="mRNA"
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100.0%; Pred. No. 1.2e-82;
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Masuho,Y., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
AU140993
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AU140993
                                                                                                                                                                                                       Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                         Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                    1532-3 Yana, Kisarazu, Chiba 292-0812, Tel: 81-438-52-3975
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EST.
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1 (bases 1 to 737)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
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                                      /tissue_type="placenta"
/clone_lib="PLACE4"
/note="Vector: pME18SFL
                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                   Location/Qualifiers
                                                                                             clone="PLACE4000626"
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Pred. No. 1.2e-82;
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University of lowa
University of lowa
375 Mewton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8256
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                        1449 ACAGGCAACGGCGAGGAGAGTGGAAGTGTGAGAGGCACCTCTGTGCAGCACCATCG 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM715855 T65 bp mRNA linear EST 28-FEB-2002 UI-E-EJO-ahj-h-11-0-UI.r2 UI-B-EJO Homo sapiens cDNA clone UI-B-EJO-ahj-h-11-0-UI 5', mRNA sequence.
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                                                                       1209 CCCATAGCTGAGAAGTGTTTTGATCATGCTGGGACTTCCTATGTGGTCGAGAAACG 1268
                                                                                                                                           1269 TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC 1328
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 765)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                              362 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGCTGGGACTTCCTATGTGGTGGGAGAAACG
                                                                                                                                                                  422 TGGGAGAAGCCCTACCAAGGCTGGATGATGTACTTGCCTGGGAGAAGCCAGC
                                                                                                                                                                                                                                      542 AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                        Gaps
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   Length 737;
                                  Indels
21.4%; Score 330; DB 1; I larity 100.0%; Pred. No. 1.3e-82; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db xref="taxon:9606"
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BM715855.1 GI:19029113
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 Query Match
Best Local Similarity
Matches 330; Conserv
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/notes="Organ: eys. Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; U1-E-E10 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAACCAACA; lens, CGATTAGCGA; eye anterior segment, AAGACCAACA; pptic nerve, CCATTAAGCG; retina, CGCGC; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI):"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU140971 AU4CE4 Homo sapiens cDNA clone PLACE4000583 5', mRNA sequence.
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1 (bases; Homo.

1 (bases 1 to 861)
Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Mishikawa,T., Nakamura,Y., Suganbi,Y. and Isogai,T., HRI human cDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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Pred. No. 1.3e-82;
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100.0%; Pred. No. 1...
... 0; Mismatches
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/clone_lib="UI-E-EJ0"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M. F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McZwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S. W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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81-438-52-3986
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/mol_type="mRNA"
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/clone="PLACE4000583"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pME18SFL3"
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/clone_lib="PLACE4"
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Best Local
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 471325; This clone has the following problem: frame shifted.

Location/Qualifiers
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94:
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse of the second of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-AUG-2004) National Institutes of Health, Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Tissue Procurement: Dr. Stefan Hansson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory
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Direct Submission
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   ACAGGCAACGGCCGAGGGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG
                                                                                                                                                                                                                                                                                                                                                                GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT
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                                                                   ACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG
                                                                                                                                                                                                                  AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
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/clone_lib="NIH_MGC_147"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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Hominidae; Homo.

1 (bases 1 to 7777)

S Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Pobo, G., Han, M. and Wiemann, S.

The German cDNA Consortium

Direct Submission

L Submitted (17-AVG-2004) MIPS, Ingolstaedter Landstr.1, D-85764

Neuherberg, GERNANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (br872); Emails wiemanna@ktz-heidelberg.de; sequenced by BWFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686K09164) is available at the RZDD Deutsches (DKFZp686K09164) is available at the RZDD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZDD for ordering:

Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZDD for ordering:

Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please tontact RZDD for ordering:

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1046 ACAGGCAACGACGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR749316 1777 bp mRNA linear HTC 19-AUG-2004 Homo sapiens mRNA; cDNA DKFZp686K08164 (from clone DKFZp686K08164).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                      806 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               986 AGAATTGGAGACCTGGGGGCAAGATAATCGAGGAAACCTGCTCCAGTGCATCGC
                                                                                                                                                                                                                                                                                                                                                                                   1209 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1269 TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          866 TGGGAGAAGCCCTACCAAGGCTGGATGGTAGGTGGTAGTTGTACTTGCCTGGGAGAAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1329 GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              926 GGACGCATCACTTCCACTTCTAGAAATAGATCCAACGATCAGGACACAAGGACATCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1389 AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1449 ACAGGCCAACGGCCGAGGAGAGTGGAGAGGCGACACACCTCTGTGCAGACCACATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="DKFZp686K08164"
/tissue_type="uterus endothel, primary cell culture"
                                                                                                                                                                                                                                               Length 7501;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                            21.4%; Score 330; DB 4; 100.0%; Pred. No. 2.5e-82; ive 0; Mismatches 0;
                                             normal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1509 AGCGGATCTGGCCCCTTCACCGATGTTCGT 1538
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                                                                                                                                           /note="Vector: pBluescriptR"
                                         /tissue_type="Placenta, n
/clone_lib="NIH_MGC_147"
/lab_hOst="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
          /clone="IMAGE:30343682"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR749316.1 GI:51476361
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                              Matches 330;
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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ACCESSION
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JOURNAL
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Rlausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Rah, S.S., Loquellano, N.A., Peters, G.J.,
Abrameon, R.D., Wullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Murny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, Y. Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Dickson, M.C., Rodriguez, A.C., Grimwood, U., Schmutz, U., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Mammalian Gene collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
All Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 198 Row: j Column: 21
This clone was selected for furl instance sequencing because it passed the following selection criteria: matched mRNA gi: 47132556 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                            BC100030 7501 bp mRNA linear HTC 02-AUG-2005 HOmo sapiens cDNA clone IMAGE:30343682, containing frame-shift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project
Direct Submission
Submission
Submitted (01-AUG-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA ibrary Preparation: Michael Brownstein / Ted Usdin
1509 AGCGGATCTGGCCCCTTCACCGATGTTCGT 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                       1106 AGCGGATCTGGCCCCTTCACCGATGTTCGT
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                         BC100030.1 GI:71679847
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1 (bases 1 to 7501)
                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens (human)
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AUTHORS CONSRIM TITLE JOURNAL

REMARK

COMMENT

FEATURES

PUBMED REFERENCE

JOURNAL

CONSRIM TITLE

CDS

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Matches 330;
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Best Local Similarity
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                                                                               1389
                                                                                                                                                                                                                                                                                                                                                                                                            1269
                                                                                                                                                                                                        GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT 1388
                                                                                                                                                                                                                                                                                                                                                                          TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCATAGCTGAGAAGTGTTTTTGATCATGCTGCTGGGACTTCCTATGTTGGTCGGAGAAACG
AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                                           AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                                                                                                                                                                                                                                                                                        TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG
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NYDADQKTGFCTPMAHESICTTNEGVMXRIGDOMDKOHDMKCTCVGNGRGEWTC
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GTFYQLGDSWEKYVHGVRYQCYCYGRGIGSWHCQDLQTYSSSGPVZVFITSTPSQDN
SHPIQWAPQPSHISKYILKWRPKNSVGRWKEATIPGHLMSYTIKGLKPGVVYEGQLI
SIQQYGHQEVTREDFTTTSTSTPVTSNTTVTTGETTPSLVATSESVTEITASSFVVSW
VSASDTWSGFRVZYELSBEGDEPQYLDLPSTATSVNIPDLLPGRKYIVWYQISDGE
QSLILSTSQTTAPDAPDPTVDQVDDTSIVVRWSRPQAPITGYRIVSPSVEGSSTEL
NLPETANSVTLSDLQPGYQYNITIAVERDESTFVVQLPITGYRLPITRSTTVSPRDLQ
FVEVTDVKYTLMTPPBSAVTGYRVDVIPVNLPGEHQGRLPITRYRPAEVTGLSPGVT
YYFKVFAVSHGRESKPLTAQQTTKLDAPTNLQFVNETDSTVLVRWTPPRAQITGYRLT
VGLTRRGQPRQYNVGBSYKYPLANLQPASSTYNGLOGSFKATGVFTTLQF
SSIPPYNTEVTETTIVITWTPAPRIGFKLGVRFNGGAPREFVTSDSGSIVVSGLTPG
GYRYTTQVLRDGQERDAPIWKVVTPLSPFTNLHLEANDDTGYLTVSWERSTTDDIT
GYRITTPTNGQQGNSLEEVVHADQSSCTFDNLSGGAPREVTSDSGSIVSTSDT
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GYRITTTPTNGQQGNSLEEVVHADQSSCTFDNLSGFGLASWSVYTYKDDKESVPISDT
GYRITTPTNGQCGNSLEEVVHADQSSCTFDNLSGFGLASWSVYTYKDDKESVPISDT
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GNTYRVGDTYERPKDSNLWDCTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRPHET
GSYNLECVCLGNGKGEWTCKPIAEKCPDHAAGTSYVGETYWKFPQGWMYNDCTCLGE
GSGRITCTSRNKCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCERHTSY
QTTSSGSGPFTDVRAAVYQPQPHQPPPGHCVTDSGVVYSVCHQMLKTQCNKQNLCT
CLGNGVSCQETAVTQTYGGNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLMCSTTSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDPHEATCYDDGKTYHYGEQNQ
KEYLGAICSCTCFGGQRGWRCDNCRRPGGEPTPEGTTGQSYNQYSQRYHQRTNTNVNC
PIECFMPLDVQADREDSRE"
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CHPVGTDEEPLQFRVPGTSTSATLTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNS
VNEGLNQPTDDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCDSSRWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDLKETQVTETSLSAOMTPENVQLTGYEVRVTEREKTGEMKEILAEDSSSVVVSGLM
VATKYEVSVYALKDTLTSREAQGVVTTLENVSPERARTVETTITISMRTKTETI
TGEQVUAVPANGQTEIQRTIKEDVRSYTITGLOGGTDYKIYLYTLINDNARSSPVVIDA
STAIDAPSNLRELATTENSLLVSWQPERARITGYIIKYEKEGSPEREVVEREREGUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSLLISWDAPATVRYYRITYGESTGAUSPYGESPLLIGQQSTVSDVPRDLEVVAATP
TSLLISWDAPATVRYYRITYGETGGAUSPVGEFTVPGSKSTATIGGLKPGVDYTITYV
AVTGRGDSPASKYE 18 INYRTEIDKESGMQVFTDVQDNS1SVKMIPSSSPVTGYRRVTTI
PKAGPGPTKTKTAGPDQTEMTIEGLQPTVEYVVSVYAQNPSGESQPLVQTAVTTIPAP
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GYYTVTGLEPGIDYDISVITLINGGESAPTTLTQQTAVPPFDLDLRFTNIGDDYMKVTW
APPPSIDLTWFLVRYSBFVANEEDVAELSISFENMAVULTNLLPGTEYVYSVSSVYSQF
ESTPLRGRQKTGLDSPTGIDFSDITANSFTVHWIAPRATITGYRIRHHPEHFSGRPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="686 (symonym: hlcc3). Vector pSport1_Sfi; host DH10B; sites SfilA + SfilB" /dev_stage="adult" /note="fibronectin 1, differentially spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="CAH18171.1"
/db_xref="GI:51476362"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 330; DB 4; ]; Pred. No. 2.5e-82; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7777;
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                                                                           1448
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REFERENCE
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SOURCE
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HSM806653
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Osanger, A., Fobo, G., Han, M. and Wiemann, S. The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Further information about the clone and the sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686M04163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ressourcenzentrum fuer Genomforschung GmbH Please contact RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone (DKFZp686M04163) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO Bapiens
BX640608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX640608.1 GI:34364616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSM806653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCGGATCTGGCCCCTTCACCGATGTTCGT 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGGCAACGGCCGAGGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAGGCAACGGCCGAGGGGGGGAGTGGGAAGTGTGAGAGGCACACACCTCTGTGCAGACCACATCG 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 7868)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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GGYNLEVCLGNGKGEWTCKPIAEKCEDHAACTSYVUGETWEKEYQGWMVDCTCLGE
GSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCERHTSV
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                                                                                                                                                                                                                                                                                                                                                                                                     codon start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="DKFZp686M04163"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:9606"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .7868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKFZp686M04163 (from clone DKFZp686M04163).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7868 bp
                                                                                                                                                                                                                                                                                                                                                    l protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hlcc3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primary cell culture"
}). Vector pSport1 Sfi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pSport1_Sfi; host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTC 20-JAN-2005
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ORGANISM

REFERENCE AUTHORS CONSRIM

COMMENT

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VGLTRRGQPRQYNVGPSVSKYPLRNLQPASBYTVSLVAIKGNQBSPKATGVFTTLQPG
SSIPPYNTSPTETTIVITYPAPARIGERLGAVBSGGGBARBERTSTBODGS
VEYVYTIQVLABCGGBADAPIVNKVVTPLSPPTNLHLBANPDTGVLTVGWBRSTTPDIT
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FVEVTDVKVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPISRNTFAEVTGLSPGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLLIGQOSTVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEF
TVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTD
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SVYAQNPSGESQPLVQTAVTTIPAPTDLKFTQVTPTSLSAQWTPPNVQLTGYRVRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEKTGPMKEI NIAPDSSSVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSP
PRRARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKPDVRSYTITGLQ
PGTDYKIYLYTLANDNARSSPVVIDASTAIDAPSNLRFLATTPNSLLVSWQPPRARITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QMI FEEHGFRRTT PPTTATPI RHR PR PY P PNVGEEI QIGHI PREDVDYHL Y PHG PGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATYNI IVEALKDQQRHKVREEVVTVGNSVNEGLNQPTDDSCFDPYTVSHYAVGDEWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMSESGFKLLCQCLGFGSGHFRCDSSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLG
NGKGEFKCDPHEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCRRPGG
EPTPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQADREDSRE"
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SHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIPGHLNSYTIKGLKPGVVYGGLI
                                                                                                                                                                    SIQQYGHQEVTRPDFTTTSTSTPVTSNTVTGETTPFSPLVATSESVTBITASSFVVSW
                                                                                                                                                                                                                         VSASDTVSGFRVEYELSEEGDEPQYLDLPSTATSVNI PDLLPGRKYI VNVYQI SEDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         YYFKVPAVSHGRESKPLTAQQTTKLDAPTNLQFVNBTDSTVLVRWTPPRAQITGYRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIIKYEKPGSPPREVVPRPRPGVTEATITGLEPGTEYTIYVIALKNNOKSEPLIGRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDELPQLVTL PHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGTSGQQPSVGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNASTGQEALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSATLTGLTR
1 A Y SQLRDQCI VDD I TYNVND TFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSET
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1328 1388 1448 ö 987 AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC 1046 1449 ACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 1508 926 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG 807 CCCATAGCTGAGAAGTGTTTTTGATCATGCTGCTGGAGTTCCTATGTGGGGGAGAAACG TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACACTTCTTAT AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC Gaps ; 21.4%; Score 330; DB 4; Length 7868; 100.0%; Pred. No. 2.5e-82; ive 0; Mismatches 0; Indels 1107 AGCGGATCTGGCCCCTTCACCGATGTTCGT 1136 1509 AGCGGATCTGGCCCCTTCACCGATGTTCGT 1538 Best Local Similarity 100. Matches 330; Conservative 1209 1269 1329 1389 927 Query Match ORIGIN qq g d ₽ ઠે 셤 ð Š ò

MVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRRARVTDATETTITISWRTKTET

Homo sapiens mRNA; cDNA DKFZp686F10164 (from clone DKFZp686F10164). CR749281. GI:51476291

Homo sapiens (human)

DEFINITION ACCESSION VERSION KRYWORDS

RESULT 12 CR749281 LOCUS

GAGRRI SCTTANR CHRGGOSYKI GDTWRR PHETGGYMLECYCLGNGKGEWTCKPLAE
GAGRRI SCTTANR CHRGGOSYKI GDTWRR PHETGGYMLECYCLGNGKGEWTCKPLAE
GAGRRI SCTTANR CHRGGOSYKI GDTWRR PHETGGYMLECYCLGNGKGEWTCKPLAE
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http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686F10164
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
1. .7885 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer 1 (bases 1 to 7885)
Kochrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
The German Consortium Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heiner-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686F10164) is available at the RZPD Deutsches /dev\_stage="adult" /note="fibronectin 1, differentially spliced" /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="DKFZp686F10164" /gene="DKFZp686F10164" 30. .7103 /gene="DKFZp686F10164" /codon start=1 Direct Submission .7885 SOUTH TITLE JOURNAL

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                               source
                                    Neuherberg, GERMANY
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Center for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp68601166) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp68601166
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Osanger, A., Fobo, G., Han, M. and Wiemann, S. The German CDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-FEB-2005) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens mRNA; cDNA DKFZp68601166 (from clone DKFZp68601166).
BX640875
BX640875.1 GI:34365169
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ASTAIDAPSNILAFLATTPNSLLVSWQPEPRARITGYIIKYEKPGSEPREWVPREREPGVT
EATTITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELPQLVTLEPHPNLHGPEILDVP
STVQKTPFVTHPGYDTGNGIQLLGTSGQQDSVCQQMIFEEHGFRTTPPTTATFIRHR
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LTRGATYNIIVEALKDQCHKKYREEVVTVGNSVNEGLINQPTDDSCPDFYTVSHYAVGD
EMERNSESGFKLLCQCLGFGGGGHFRCDSSRWCHDNGYNYKIGEKWDRQGENGOMNSCT
CLGNGKGEFKCDPHEATCYDDGKTYHVGEQWQXEYLGAICSCTCFGGGRGWRCDNCRR
PGGEEPSPEGTTGQSYNQYSQRXHQRTNTNVNCPIECFMPLDVQADREDSRE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                   PLIGRKKTDELPQLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGTSG
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PHGPGLNPNASTGQEALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSA
                                               AVGDEWERMSESGFKLLCQCLGFGSGHFRCDSSRWCHDNGVNYKIGEKWDRQGENGQN
MSCTCLGNGKGEFKCDPHEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCL
NCRRPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNYPIECFMPLDVQADREDSRE"
                                                                                                                             TLTGLTRGATYNI I VEALKDQQRHKVRBEVVTVGNSVNEGLNQPTDDSCFDPYTVSHY
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/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
pH10B; sites SfIIA + SfIIB"
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/protein_id="CAE45932.;
/db_xref="GI:34365170"
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Best Local Similarity Matches 330; Conserv

Conservative

21.4%; but 100.0%; Pr

; Score 330; DB %; Pred. No. 2.6 0; Mismatches

2.6e-82; DB 4;

Length 8411; Indels

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AU140802 AUG-2002 AUG-2002 AU140802 PLACE4 Homo sapiens cDNA clone PLACE4000266 5', mRNA
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                                                                                                   434 CCCATAGCTGAGAAAGTGTTTTGATCATGCTGCTGGGGGCTTCCTATGTGGTGGAGAAACG 375
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genomics@hri.co.jp

HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix

HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix

Vesearch Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Qualifiers
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1 (bases 1 to 734)

Ota, T., Suutki, Y., Saito, K., Ishii, S., Yamamoto, J., Sugiyama, T.

Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y. and Isogai, T.

Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y. and Isogai, T.

HRI human cDNA project (Ota, T., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sugiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y., Isogai, T.

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory
                                                                                                                                                                                         1329 GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT
                                                                                                                                                               TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC
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                           1; Indels
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
17El: 81-438-52-3975
Fax: 81-438-52-3986
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99.7%; Pred. No. 2.5e-82;
iive 0; Mismatches 1;
      Pred. No. 2.2e-82;
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    Best Local Similarity 99.7
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db24a08.x1 Soares pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697174 3' similar to gb:x02761_cds1 FIBRONECTIN PRECURSOR AI095589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tunor Gene Index
Unpublished (1997)
Contact: Robert Stausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.lnh.gov) for further information.
Insert Length: 1871 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 446.
Location/Qualifiers
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1 (Dases 1 to 465)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AI095589/c LOCUS DEFINITION

RESULT 14

ACCESSION VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS TITLE

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PEATURES

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Aay84004 A Aay84005 A Aax12892 T Aap50620 S	Aar10198 & Aab74940 M Aay84007 A Aaw21723 P Aaw21727 S Aay84006 A Aar12884 M	Aay25020 S Abb80012 S Abg74199 R Aar10200 S Aar10197 S Aar10195 S	Aay50870 S Aay99593 S Aaw86144 D Aab01296 A Aar06377 S Aaw21725 M Aaw21725 M	Aeb93425 S Aaw86143 S Aab01295 W Aar12889 S Aar12885 F Aar12891 S Aar20200 C	$\omega \otimes \omega \alpha$
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## ALIGNMENTS

RESULT 1 ADL92189 harvesting; recombinant; host cell; N-terminal leader peptide; pre-peptide; lantibiotic; post-translational modification; pharmaceuticals; vaccine; immunogenic. 24-MAY-2002; 07-FEB-2003; 04-DEC-2003. WO2003099862-A1 Unidentified Streptokinase protein sequence. ADL92189 standard; protein; 413 AA 26-MAY-2003; 2003WO-NL000389 20-MAY-2004 ADL92189; (-ONAN) gy, APPLIED NANOSYSTEMS BV Leenhouts CJ, 2002EP-00077060. 2003US-00360101. (first entry) Kuipers OP, Driessen AJM;

Harvesting a desired polypeptide produced by a recombinant host cell, for producing pharmaceuticals, comprises selecting a recombinant nucleic acid

PPXRXPXPXPXPXPXPXPXPXXPXXPXXPXXPXDXAXD

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The invention relates to a novel method for harvesting a (poly) peptide produced by a recombinant host cell. The novel method involves selecting a cell comprising a first nucleic acid encoding a leader peptide and a second nucleic acid fragment encoding the desired (poly) peptide and a first and second fragments are within the same open reading frame of the first nucleic acid and the leader peptide is functionally equivalent to an N-terminal leader peptide found with the pre-peptide of a lantibiotic. The host cells and nucleic acids are useful for producing, harvesting and post-translational modification of polypeptides. The polypeptides may be used in the production of pharmaceuticals, e.g. as antigen for vaccine or immunogenic composition. This sequence represents a polypeptide relating to the novel method of the invention.
comprising nucleic acid fragments encoding a leader peptide and the polypeptide.
                                                                                4; Page 82-83; 109pp; English
                                                                                   Claim
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Sequence 413 AA;

152 212 272 332 100 392 120 452 140 512 160 572 180 632 200 692 220 92 20 40 9 80 AGCGTTGCTGCTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGGCAAGGCTTAAGTCCAAAATCA AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACTACTTTGAGGTC GluTyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGlyLeuLys AspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeu GCTCAAGCACAAAGCATTTTAAACAAAACCACCCAGGCTATACGATTTATGAACGTGAC ATAGCTGGTCCTGAATGGCTACTAGATCGTCCTTCTGTAAATAACAGCCAATTGGTTGTT AAACCATTIGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG ValArgValArgProTyrLysGluLysProlleGlnAsnGlnAlaLysSerValAspVal GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT 413 383 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-940-235-9 (1-1541) x ADL92189 (1-413) 1.13e-178 1984.00 100.00\$ 100.00\$ 73.05\$ Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: 33 93 153 41 213 61 273 101 121 141 181 21 81 393 513 633 333 453 161 573 201 Score: ò ద 8 ያ ያ 8 & 8 8 & B & 8 6 6 6 중 염 ò q ò

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DNA encoding a polypeptide which region of streptokinase - useful treat myocardial infarction.
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29-SEP-1993;
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       Nucleic acid comprising a sequence encoding amino acids 14-414 of streptokinase, which binds to plasminogen and does not have a sequence comprising amino acids 60-414 is new. The polypeptide pref. comprises amino acids 244-352, 1-352, 1-352, 20 244-414. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                         AGCGTTGCTGCTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC
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                                                                                                                                                                                                                                                    induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; an nucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host call transformed with the expression vector of (3). The pharmaceutical composition comprising a
                                                                                                                                                                                                                                                                                                                                                                                               ACCAACCGTATCATAACCGTTTATATGGCCAAGCGACCGAAGGAGAGAAATGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence represents native streptokinase (nSK). (Updated on 17-OCT-2003 to
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Mutant streptokinase thrombolytic agent.
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                                       N-PSDB;
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                  The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence represents native SK. SK is a secretory protein of plasmin (HPIM), which is a serine protease able to catalyse the hydrolysis of them the protease able to catalyse the hydrolysis of them in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as a cute myocardial infarction. Compared with wild type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen. (Updated on 17-OCT-2003 to standardise OS field)
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                         AspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAsp
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thrombolytic therapy.
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dysgalactiae subsp. equisimilis

EP1024192-A2

02-AUG-2000

23-DEC-1999; 99EP-00310541

24-DEC-1998; 98IN-DE003825

(COUL ) CSIR COUNCIL SCI IND RES

Sahni Yadav **3** 0 Kumar R, Roy ú Rajogopal <u>,</u>7 Nihalani Á Sundaram

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N-PSDB; WPI; 2000-516032/47

Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin domains of human fibronectin. binding

Fig 58pp; English.

This sequence represents the human Streptococcus equisimilus streptokinase protein sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, fibrin binding regions of human fibronectin, which are from fibrin binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a and

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pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG: The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of aardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 12-SBP-2003 to standardise OS field)
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GCTCAAGCACAAAGCATTTTAAACAAAACCACCCAGGCTATACGATTTATGAACGTGAC 692

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1052 1112 1172 360 260 280 932 300 992 SerSerlleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu 240 GluLysProTyrAspProPheAspArgSerHisLeuLysLeuDheThrIleLysTyrVal TITACITACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAATCTGGTCTG **AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG** GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis. The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical Streptokinase and maltose binding protein fusion protein. Streptococcus dysgalactiae subsp. equisimilis. Ź N-terminally deleted streptokinase. Example; Page 48-51; 73pp; English AAY24797 standard; protein; 795 98WO-US026694 97US-0069497P (first entry) (HARD ) HARVARD COLLEGE CATTTAGCT 1181 ||||||||||| HisLeuAla 383 WPI; 1999-395183/33. N-PSDB; AAX80497 WO9931247-A1 15-DEC-1998; 15-DEC-1997; 26-AUG-1999 24-JUN-1999 Synthetic 281 241 301 321 1113 1173 381 1053 AAY24797; 221 753 813 261 873 933 993 Ġ, Reed ( RESULT 8 AAY24797 à 셤 셤 ò 셤 ò 셤 8 셤 셤 셤 셤 ò ð Š ð

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Best I
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Fibrin-binding streptokinase;
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                                                     30-APR-1991.
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                          15-NOV-1989;
                                                                                US5011686-A.
                                                                                                                                                                                                                                                                                      fusion
                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 531 AA
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fusion protein.
87US-00099242
                          89US-00437769
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                                                                                                                                                                                                                                                                                     conjugate.
                                                                                                          /label= streptokinase
                                                                                                                                                              /label= FB
                                                                                                                                   label= FB monomer
                                                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                               monomer
                                                                                                                                                                                                                                                          fibrinogen;
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GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1112
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SerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasma clot, hydrolysis, haemolytic Streptococcus; plasminogen; plasmin, serine protease, fibrin; blood clot, thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction;
                     TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG
                                                                                                                                                     GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGGCTAGCGAACGTAAC
                                                                                                                                                                                              TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTTACAACAATCTC
                                                                                                                            GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal
                                                                                                          GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant streptokinase polypeptide - useful as plasmin-resistant
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Misc-difference
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Synthetic.
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                                                  Imparting injectable fibrinolytic agent - with affinity for intravascular thrombus, by linking agent to fibrin binding domain.
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                                                                                                      The conjugate comprises an FB-FB dimer linked to streptokinase The FB fragment has selective affinity for fibrin, low affinity for fibrinogen, and minimal immunogenicity, imparting thrombus- targetting capability. See also AAR11821 and AAR11828
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                                                                                    Disclosure; Fig 5; 18pp; English
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the Pro58-Ly859-Ser60-Ly861 segment of the corresponding mative SK is replaced by another amino acid. The present sequence is mutant SK K59E. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPlg) to plasmin (HPlm), which is a serine protease able to catalyse the hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen
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07-DEC-1990;
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Factor Xa-cleavable streptokinase-IEGR-hirudin.
                             BRITISH BIO-TECHNOLOGY LTD
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(first entry)
                                                            89GB-00027722
90WO-GB001911
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                                                                                                                                                                                                                                                                                                                                                                                thrombolysis
                                                                                                                                                                                                                                                                                                                                                                                            blood clotting; coagulation; fibrinolysis;
                                                                                                                                                                                                                                     /label= linker
/note= "factor Xa cleavage
                                                                                                                                                                                                                                                                  /label= streptokinase
415. .418
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                       /label= hirudin
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The protein is a recombinant product of a gene fusion construct. The sequence of the synthetic hirudin HV-1 genes was designed based on the published amino acid sequence (Dodt J., et al FEBS Letters 165 180 (1984)). The sequence of streptokinase was obtd. from FCR amplified chromosomal DNA from S. equisimilis ATCC 10009 or ATCC 9642. The primers used for the PCR were based on the pub- lished DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]). The two sequences were used to construct an expression vector in which the streptokinase gene is linked to the hirudin gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also ARR12887-R12889, AAR12891-R12894 and AAR12885. (Updated on 25-MAR-2003 to correct PA field.)
                                                                         Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                           Disclosure; Page 96; 115pp; English
WPI; 1991-208151/28.
N-PSDB; AAQ12490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 483 AA;
                                                                                                                              prophylaxis.
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## 483 401 17 52 38 8 Length: Matches: Conservative: Mismatches: Indels: 4.46e-178 1978.00 82.28% 78.94% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

1 IleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal 21 SerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeuLysPhePheGluIle 41 AspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer 213 AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACTTTGAGGTC ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC IleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAsp AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT GTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGGCAAGGCTTAAGTCCAAAATCA 141 ValArgValArgProTyrLysGluLysProIleGlnAsnGlnAlaLysSerValAspVal 33 ATAGCTGGTCCTGAATGGCTACTAGATCGTCCTTCTGTAAATAACAGCCAATTGGTTGTT AGCGTTGCTGGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTT US-09-940-235-9 (1-1541) x AAR12522 (1-483) 333 101 93 153 61 273 81 393 121 453 8 6 6 6 ð 셤 셤 6 B 6 셤 Š 요 당 ð 셤 δ

573 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 632

qq	181	AspThrIysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeu 200
È	633	
qq	201	AlaGinAlaGinSerileLeuAsniysThrHisProGlyTyrThrileTyrGluArgAsp 220
Š	693	TCCTCAAICGTCACTCATGACAAIGACATTITCCGTACGATTTTACCAAIGGATCAAGAG 752
q	221	SerSerlieValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu 240
Ġ	753	TITIACITIACCGIGITIAAAAATCGGGAACAAGCITIATIAGGATCAATAAAAAATCTGGTCTG 812
qq	241	PheThrTyrHisValLysAsnArgGluGlnAlaTyrGluIleAsnLysLysSerGlyLeu 260
ò	813	AATGAAGAAATAAACAACTGACCTGATCTCTGAGAAATATTAACGTCCTTAAAAAAGGG 872
e G	261	AsnGluGluileAsnAsnThrAspLeulleSerGluLysTyrValLeuLysLysGly 280
ઠે	873	GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 932
අු	281	GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrileLysTyrVal 300
ઠે	933	GATGICGATACCAACGAATIGCTAAAAAGIGAGCAGCTCTTAACAGCTAGCGAACGTAAC 992
q	301	AspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsn 320
È	993	TTAGACTICAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTACAACAATCTC 1052
qq	321	
à	വ	GATGCTTTTCGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1112
q	341	AspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAsp 360
ò	1113	
a	361	ThrasnargileilethrvalTyrMetGlyLysargProGluGlyGluAsnalaSerTyr 380
ઠે	1173	CAITTAGCTGGTGGTGGCCAGGCGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGAT 1232
q	381	HisbeualaTyrAspLysAspArgTyrThrGluGluGluArgGluValTyrSer 398
ò	1233	CARGCTGCTGCGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGCCTGG 1292
eg G	399	TyrLeuArgTyrThrGlyThrProlleProAspAsnProAsnAspLysIleGluGlyArg 418
à	1293	ATGATGGTAGATTGTACTTGCCTGGGAGAAGGCGGA 1331
q	419	::::: ValValTyrThrAspCysThrGluSerGlyGlnAsnLeuCysLeuCysGluGlySerAsn 438
ò	1332	CGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGA 1391
q	439	ValCysGlyGlnGlyAsnLysCysIle 447
È	1392	ATTGGAGACACCTGGAGAAAAAGATAATCGAGAAACCTGCTCCAGTGCATCTGCACA 1451
qq	448	LeudlySerAspGlyGluLysAsnGlnCysValThr 459
Š	1452	GGCAACGGCCGAGGAGAGTGGAAGTGTGAGGCACACTCTGTGGAGACCACACATCGAGC 1511
qq	460	GlyGluGly
È	1512	GGATCTGGCCCTTCACCGATGTT 1535
дg	470	AsnAspGlyAspPheGluGluIle 477
RESUL AAW21 ID XX	T 12 728 AAW21728	standard; protein; 813 AA.
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01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the wild type plasminogen-binding fragment of streptokinase. This fragment was used in the design of a modified streptokinase. This fragment was used in the design of a modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, opt. as a bolus rather than by continuous infusion. (Updated on 17-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 12-13; 65pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified forms of streptokinase resistant to enzymatic cleavage - useful as thrombolytic agents in treating thrombosis and in medical equipment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-065469/06.
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ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
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                                                                                                 LysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeu
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            dysgalactiae
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blood clot; bolus; maltos
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                                                                                                                                                                                                                                                                                                     This sequence represents a fusion protein between maltose-binding protein and the plasminogen-binding fragment of streptokinase. This fusion protein was used in the design of modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, optionally as a bolus rather than by continuous infusion. (Updated on 17-0CT-2003 to standardise OS field)
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                                                                                                                                                                                                                                            Modified forms of streptokinase resistant to enzymatic cleavage - useful as thrombolytic agents in treating thrombosis and in medical equipment.
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          1. .381
| Jabel= Maltose binding protein.
| note= "acts as blocking group"
382. .1194
| label= Streptokinase
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                                                                                                                                                                                                                                                                                  Example 1; Page 11-12; 65pp; English.
Location/Qualifiers
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                                                                                                                            07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                           The invention relates to a method for identifying and quantifying one or CC more proteins in complex mixtures by selectively isolating peptides not containing histidine mor arginine (NHNR peptides) from each protein, and determining the relative concentration of one or more proteins in CC different samples from the ratio between the areas of estimated CC theoretical spectra for each NHNR peptide labeled with different isotopes in each sample. The method comprises: (a) enzymatically or chemically CC hydrolyzing the sample or samples of proteins; (b) chemically modifying CC history in step (a); (c) isolating the NHNR peptides by cation exchange CC obtained in step (a); (c) isolating the NHNR peptides by cation exchange chromatography from the mixture of peptides obtained in step (b); (d) differential isotopic labeling of protein contained in step (c); (e) differential isotopic labeling of protein step (c); (e) differential isotopic labeling of protein containing at least a portion of the samples; and (f) relative quantifying of mixing at least a portion of the samples; and (f) relative quantifying of che estimated theoretical spectra of the pair of NHNR peptides containing at least a portion of step (e) from the ratio between the careas of estimated theoretical spectra of the pair of NHNR peptides (c) identified in step (d). Also described is a kit for the identification and quantifying proteins, such as those with vaccinal, therapeutic or containing proteins, such as those with vaccinal, therapeutic or containing protein, which is used in an example from the present a containing protein, which is used in an example from the present a convention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC 152
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                                                                                                  Non-immunogenic; epitope; T-cell; immunogenicity; immune system; immunogl bulin; therapeutic; streptokinase.
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Mismatches:
Indels:
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                                                                              Streptokinase (SK) protein sequence
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AAW86143 standard; protein; 414
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97GB-00016197.
97GB-00025270.
97US-0067235P.
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                                             (revised)
(first entry)
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Best Local Similarity:
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31-JUL-1997;
28-NOV-1997;
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14-APR-1998;
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03-MAR-1999
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Search completed: January 28, 2006, 02:08:00 Job time: 126.195 secs

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Result
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-DB=1ssued_patents_AA_-OFMT=fastan_-SUFFIX=rai_-MINMATCH=0_1_LOOPCI=0
-LOOPEXT=0_-UNITS=bits_START=1_-SUD=1_-MATRIX=blosum62_-TRANS=human40.cdi
-LIST=45_-DCCALIGN=200_-THR_SCORE=pct_-THR_MAX=100_-THR_MIN=0_-ALIGN=15
-MODE=LOCAL_OUTFMT=pto_-NORM=ext_-HEAPSIZE=500_-MINLEN=0_-MAXLEN=2000000000
-USER=US09940235_@CGN_1_1_159_@runat_27012006_144219_27602_-NCPU=6_-ICPU=3
-NO_MMAP_LARGEQUERY_-NEG_SCORES=0_-WAIT_-DSPBLOCK=100_-LONGLOG_-DEV_TIMEOUT=120_-WARN_TIMEOUT=30_-THREADS=1_-XGAPOP=10_-XGAPEXT=0.5_-FGAPOP=6_-FGAPEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DELEXT=7_
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Maximum DB
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Perfect score:
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Match
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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              US-08-560-098A-52

US-09-211-542A-2

US-07-854-596B-47

US-08-488-940-3

US-08-488-940-1

US-07-854-596B-26

US-07-854-596B-19

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Sequence 6, Appli
Patent No. 5240845
Sequence 52, Appli
Sequence 2, Appli
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## ALIGNMENTS

RESULT 1 US-10-360-101-264

Sequence 264, Application US/10360101 Patent No. 6861236

PATENT NO. 6861336

PATENT NO. 6861366

GENERAL INFORMATION:

APPLICANT: Moll, Gert N.

APPLICANT: Hoenhouts, Cornelis J.

TITLE OF INVENTION: Export and modification of FILE REFERENCE: 2183-5673

CURRENT APPLICATION NUMBER: US/10/360,101

CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: EP 02077060.8

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 309

COPTWARDE: DATAITON STREET US-09-940-235-9 (1-1541) x US-10-360-101-264 (1-413) Query Match: Best Local Similarity: Score Pred. No.: Alignment Scores: Percent Similarity: US-10-360-101-264 SOFTWARE: PatentIn version 3.1 SEQ ID NO 264 LENGTH: 413
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: sequence of streptokinase 2.88e-192 1984.00 100.00% 100.00% 73.05% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: of (poly) peptide in the lantibiotic way 413 383 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09211542A
Patent No. 6210677
GENERAL INFORMATION:
TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 lleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal
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Mismatches:
Indels:
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Matches:
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FILING DATE: 15-December-1998
CLASSIPICATION: 1653
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: ALCOTTEN, Stringel, Harriet M. REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)443-9292
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ξ
                                                                                                                                                                                   3: BROMBERG & SUNSTEIN, LLP
125 Summer Street
                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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100.00%
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73.05%
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SEQUENCE CHARACTERISTICS:
LENGTH: 414 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
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amino acid
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                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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RESULT 3
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CURRENT APPLICATION DATA:
 APPLICATION NUMBER:
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KOICHI; ONO, KENJI; SAKATA, YASUYO; UENOYAMA,
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Alignment Scores:  2.98e-192 Length: 440 Score: 1984.00 Matches: 383 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 73.05% Indels: 0	107	LENGTH TYPE: STRANDI	NI		PRIOR APPLICATION DATA:  APPLICATION NUMBER: P 44 40 892.7  FILING DATE: 17-NOV-1994  ATTORNEY/AGENT INFORMATION:	SOFTWARE: Patenti CURRENT APPLICATION I APPLICATION NUMBER FILING DATE: 17-N	COMPUTER MEDIUN COMPUT OPERAT	CITY: Washington STATE: DC COUNTRY: USA ZIP: 20005	NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: ADDRESSEE: Evenson, McKeown, Edwards & Le STREET: 1200 G Street, N.W., Suite 700	HEINZEL- STEFFENS NVENTION:	Sequence 52, Application US/08560098A ; Patent NO. 5976841 ; GENERAL INFORMATION: ; APPLICANT: WNENDT, Stephan	Db 381 HisheuAla 383 RESULT 4	1173 CATTTAGCT 1181	Qy         1113 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAATGCTAGCTA	Qy 1053 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1112	321 LeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeu	Ob 301 AspValAspThrAsnGluLeuLeuLysSerGluGinLeuLeuThrAlaSerGluArgAsn 320 Qy 993 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 1052	Db 281 GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal 300 Qy 933 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCTCTTAACAGCTAGCGAACGTAAC 992
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153 GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA	Qy 93 AGCGTTGCTGGTACTGTTGACGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATC 152	TAGCTGGTCCTGAATGGCTACTAGATCGT	73.05% Indels: 2 Gaps: 1) x IIS-09-211-542A-2 (1-795)		. PE	; SEQUENCE CHARACTERISTICS: ; LENGTH: 795 amino acids ; TYPE: amino acid ; TOPOLOGY: linear	; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (617)443-9292 ; TELEPAX: (617)443-0004 ; INFORMATION FOR SEO 1D NO: 2:	; ATTORNEY/AGENT INFORMATION: ; NAME: Attorney, Strimpel, Harriet M. ; REFERENCE/DOCKET NUMBER: 1874/111 ; REFERENCE/DOCKET NUMBER: 1874/111			; COMPUTER READABLE FORM: ; MEDIUM TYPE: Flappy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS	CITY: Bc STATE: M COUNTRY: ZIP: 021	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: BROMBER STREET: 125 Summer		RESULT 5 US-09-211-542A-2 ; Sequence 2, Application US/09211542A	Oy 1173 CATTTAGCT 1181	Qy 1113 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGCTA	
RESULT 6 US-07-854- ; Sequence	g Q	DB QY	Ωy	Db Oy	D Q	D Oy	4d 45	D &	P &	95 Q	Db Qy	D Q	Db Qy	Qу	B 8	B 6	} B &	S B
4-596B-47 ce 47, Application US/07854596B	1173 CATTTAGCT 1181         762 HisLeuAla 764	1113 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGCTA	1053 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1112 	993 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCCTACAACAATCTC 1052 	933 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 992 	873 GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 932 	813 AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG 872 	753 TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 812 	693 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 752 	633 GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 692 	573 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 632 	513 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 572 	453 GTGCGCGTTAGACCATATAAAGAAAAACCAATACCAAACCAAGCGAAATCTGTTGATGTG 512 	393 AAAGATGGTTAGCGTAACCTTGCCGACCCAACGTGTCCAAGAATTTTTGCTAAGCGGACAT 452		ANUSCLAI CAMANACHAITHA I GCIANGEICHAG FANGACHACHTIGHGEIC 		422 AspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer 441

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REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,3:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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GENERAL INFORMATION:
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CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/854,596B
FILING DATE: 03-UW-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           No.:
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                        LeuGlySerAspGlyGluLysAsn----
                                                                                                                         :::::: ||||||||| ||| ValValTyrThrAspCysThrGluSerGlyGlnAsnLeuCysLeuCysGluGlySerAsn 438
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                                                                                                                                                                                                                                                    CATTTAGCTGGTGGTGGCCAGGCGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGAT 1232
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                                                 ATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACA 145:
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                          -GlnCysVal---Thr 459
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Oy  93 AGCGTTGCTGGTACTGTTGAOGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC	940-235-9 (1-1541) x US-08-488-940-3 (1-813)  33 ATAGCTGGTCCTGAATGGCTACTAGATCGTCCTTCTGTAA	Algument Scores:  2.4e-190 Length: 813 Score: 1966.50 Matches: 382 Percent Similarity: 99.74% Conservative: 0 Best Local Similarity: 99.74% Mismatches: 0 Ouery Match: 72.40% Indels: 1 DB: 1 Gaps: 1	; STRANDEDNESS: not relevant ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-488-940-3	; TELERAX: 617/542-8906 ; TELEX: 200154 ; INFORMATION FOR SEQ ID NO: 3: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 8.13 amino acids ; TYPE: amino acid	REGISTR REFEREN TELECOMMU TELEPHO	; APPLICATION NUMBER: US/08/88,940 ; FILING DATE: 09-JUN-1995 ; CLASSIFICATION: 514 ; ATTORNEY/AGENT INFORMATION: ; NAME: FIRSEY Janis K	COMPUTER: 1BM PC com OPERATING SYSTEM: PC SOFTWARE: Patentin R CURRENT APPLICATION DAT	COUNTRY: U ZIP: 02110 COMPUTER READ MEDIUM TYPE	STREET: 2 CITY: Bos STATE: MA	TITLE OF INVENTION: PLASMIN-RES NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:	; Sequence 3, Application US/08488940 ; Patent No. 5854049 ; PEREAL INFORMATION: ; APPLICANT: Reed Giv I.	RESULT 7 US-08-488-940-3	1512 GGATCTGGCCCCTTCACCGATGTT	
Qy 1173 CATTTAGCT 1181  Db 380 HisLeuAla 382  RESULT 8 US-08-488-940-1 ; Sequence 1, Application US/08488940 ; Patent No. 5854049 ; GENERAL INFORMATION: ; APPLICANT: Reed, Guy L. ; TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE ; NUMBER OF SEQUENCES: 20	340 1113 360	Qy 993 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 1052	Db 280 GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal 299  Qy 933 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCGAACGTAAC 992	Qy 813 AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG 872	Qy 753 TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 812	Qy 693 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 752	Qy 633 GCTCAAGCACAAAGCATTTTAAAACAAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 692	573 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA	Qy 513 GAATATACTGTACAGTTTAACTCCCTTAAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 572	Qy 453 GTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG 512	Qy 393 AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCCAAGAATTTTTGCTAAGCGGACAT 452	Qy 333 ATTGATTTTGCTAACCGATGCAACCATTACTGATACGGCAAGGGTCTACTTTGCTGAC 392	81	Оу 273 ААСССТАТТСААСААСБАТТСАТССТВАССТССАСАСТВАССАССВССТВСТТТСАССТС 332

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-UUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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STREET: 225 F:
CITY: Boston
STATE: MA
COUNTRY: USA
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
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TELEX: 200154
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TELEFAX: 617/542-8906
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Matches:
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           STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
                                                                                                                                                              CORRESPONDENCE ADDRESS:
  CURRENT APPLICATION DATA:
                                                                                                                      STREET: Ten S
                                                                                                                                                  ADDRESSEE: Dr. John J. McDonnell
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDONNELL, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPAN: 312-715-1000
TELEPAN: 312-715-1234
TELERA: 910-221-5317
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
TENUTUME AT SEMICE STATES
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
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; Sequence 19, Application US/07854596B
; Patent No. 5434073
; GENERAL INFORMATION:
; APPLICANT: Dawson, Keith M
; APPLICANT: Hunter, Michael G
; APPLICANT: Czaplewski, Lloyd G
; TITLE OF INVENTION: Proteins and nu.
; NUMBER OF SEQUENCES: 73
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US-07-854-596B-19
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TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 435 amino actic
                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/07/854,596B
FILING DATE: 03-UNN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1034
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ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive,
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3Y: linear
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Query
DB:
            Percent Similarity:
Best Local Similari
Query Match:
                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC_DOS/MS_DOS
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDCDAME! John J
REGISTRATION NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPAX: 312-715-1000
TELEPAX: 312-715-1000
TELEPAX: 910-221-331
INFORMATION FOR SEQ ID NO: 15:
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US-07-854-596B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/07854596B
Patent NO. 5434073
GEMERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCE CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

Ornbesses:

Dr. John J. McDonnell

Numbersses:

Wacker Drive,
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                   No.:
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CITY: C
                                                                                                                                      LENGTH: 440 amino acids TYPE: amino acid TOPOLOGY: linear
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US-09-940-235-9 (1-1541) x US-07-854-596B-15 (1-440)

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RESULT 12
US-07-854-596B-43
; Sequence 43, App
; Patent No. 54340
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US-07-854-596B-43
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STREET: Ten South Wacker Drive, Su
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins at
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
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TELEFAX: 312-715-1234
TELEFX: 910-221-5317
INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDONNell, John J
REGISTRATION NUMBER: 26,949
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prof
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Proteins and n
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEB: Dr. John J. McDonnell
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TELECOMMUNICATION INFORMATION:
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STATE: IL
COUNTRY: U
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RESULT 13
US-07-854-596B-28
; Sequence 28, Application Us
; Patent No. 5434073
; GENERAL INFORMATION:
; APPLICANT: Dawson, Kei

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GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                ADDRESSEE: Dr. John J. McDonnell STREET: Ten South Wacker Drive, CITY: Chicago STATE: LL COUNTRY: USA ZIP: 60606
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/07/854
PILING DATE: 03-UN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
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SOFTWARE: PatentII
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                    LysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis
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RESULT 14 US-07-854-596B-35

Sequence 35 Patent No.

35, Application 5. 5434073

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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Mismatches:
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                                                                                                 Length:
Matches:
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              TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                               2.53e-187
1937.50
88.64%
86.86%
71.34%
   LENGTH: 1194 amino acids
                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                             US-08-488-940-18
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GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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                                      TCCTCAATCGTCACTCATGACAATGACATTTTTCCGTACGATTTTACCAATGGATCAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boscon
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-JUN-1995
CIASSIFICATION: 11.995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMÁTION:
APPLICANT: Reed, GUY L.
TITLE OF STAVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pieh & Richardson P.C.
STREET: 2½ Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELERX: 617/542-8906
TELEX: 20011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
10S-08-488-940-18
; Sequence 18, Application US/08488940
; Patent No. 5854049
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 3
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512 540 572 560 692 900 812

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1173 CATTTAGCTGGTGGTGGCCAGGCGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGAT 1232
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779 TyrLeuàrgTyrThrGlyThrProlleProAspAsnProAsnAspLysAsnAsnSerGln 798
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799 LeuValValSerValAlaGlyThrValGluGLyThrAsnGln-AspIleSerLeuLysPh 818
1347 TCTAGAAATAGATGCAACGATCAGG 1371
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Search completed: January 28, 2006, 02:40:58 Job time : 40.9832 secs

Perfect score:

Sequence:

OM nucleic

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Run

Scoring table:

Minimum DB a

Searched:

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Sequence 264, Application US/10360101

Sequence 264, Application US/10360101

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
TITLE OF INVENTION: 2013-05-07

PRIOR PILING DATE: 2003-02-07

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 309

SEQ ID NOS: 309

SEQ ID NO 264
                                                                       1069, Ap
4, Appli
                                                                                                                  363, App
1075, Ap
8, Appli
2, Appli
64, Appl
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US-10-741-601-356

US-10-741-601-363

US-10-741-601-363

US-10-741-601-0175

US-10-79-733-8

US-10-236-392-2

US-10-171-311-64

US-10-236-392-2

US-10-171-311-64

US-10-37-938-98

US-10-177-238-677

US-10-477-238-677

US-10-477-173-677

US-10-471-161-3

US-10-741-601-357

US-10-741-601-357

US-10-741-601-366

US-10-741-601-366

US-10-741-601-37

US-10-741-601-366

US-10-741-601-366

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US-10-741-601-366

US-10-741-601-366

US-10-741-601-369

US-10-287-436A-1137

US-11-0-40-130-28

US-10-711-601-360

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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.21e-177
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                                                                  Percent Similarity:
Best Local Similarity:
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DB:
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OP CGRT 1/USFTO SPOOL P/USO9940235/runat 27012006_144219_27635/app_query.fasta_1.7708
-0-6/GRT 1/USFTO SPOOL P/USO9940235/runat 27012006_144219_27635/app_query.fasta_1.7708
-0-8-Published Applications AA Main - QFWT=Fastan - SUFFIX=reapbm - MINMATCH=0.1
-DGPCL=0 - LOOPEXT=0 - UNITS=blits - START=1 - END=-1 - MATRIX=bloosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=00 - THR_SCORE-pct - THR_NAX=100
-TRANS=human40.cdi - LIST=45 - DOCALIGN=00 - NORM=ext - HRAPSIZE=500 - MINLEN=0
-THR_NIN=0 - ALIGN=15 - MODE=LOCAL - OUTFWT=pt - NORM=ext - HRAPSIZE=500 - MINLEN=0
-NORM=6 - LICPU=3 - NO MMAP - LARGOUERT - NEG GCMS=0 - WAIT - DSPBLOCK=100
-LONGIAG - DEV TINEOUT=20 - WARN TINEOUT=30 - THRRADS=1 - XGAPEXT=0.5
-EGAPEXT=7 - YGAPEXT=7 - YGAPEXT=0.5 - DBLOP=6 - DBLEXT=7
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                                                                                                                                                   January 28, 2006, 01:51:16; Search time 100.774 Seconds (without alignments) 12778.538 Million cell updates/sec
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Sequence 1066, Ap
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                        protein search, using frame_plus_n2p model
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US-09-940-235-2
US-10-988-943-1
US-10-300-215-252
US-10-300-215-253
US-09-919-703-12
US-10-444-194A-52
US-10-144-194A-52
US-10-144-194A-52
US-10-741-601-354
US-10-741-601-1066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
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2716
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TYPE: PRT ORGANISM: Streptococcus equisimilis
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CATTIAGCT 1181
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Best Local Similarity:
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                   AspleuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer
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                                                                                   AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA
                                                                                               AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC
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Sequence 2, Application US/09940235
; Sequence 2, Application US/09940235
; Publication Wo. US20030059921A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Sundaram, Vacint
APPLICANT: Sundaram, Vacint
APPLICANT: Nihalani, Deepak
APPLICANT: OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
ITILE OF INVENTION: PROTEIN
ITILE OF INVENTION: NUMBER: US/09/940,235
CURRENT APPLICATION NUMBER: 109/471,349
PRIOR FILING DATE: 1998-12-23
PRIOR PLING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 414
WADDE: NUMBER: N 152 GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA 212 272 AAGGCTATTCAACAACTTGATCGCTAACGTCCACAGTAACGACGACTACTTTCAGGTC 332 392 92 20 40 9 80 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC 1 lealaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal 213 AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT 33 ATAGCTGGTCCTGAATGGCTACTAGATCGTCCTTCTGTAAATAACAGCCAATTGGTTGTT 414 383 0 0 0 0 Conservative: Mismatches: Indels: US-09-940-235-9 (1-1541) x US-09-940-235-2 (1-414) Length: Matches:

OY 453 GIGGGGGITAGACCAIATAAAGAAAACCAATACAAAACCAAGGGAAATCIGITGAIGIG 512	Pred. No.:
	Score: Percent Similarity:
OY 513 GAATATACTGTACAGTTTACTCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 572	Best Local Similarit Query Match:
	DB:
Qy 573 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACAACTAGAATTACTA 632	US-09-940-235-9 (1-1
	Qy 30 ATGATA
	Db 1 Metile
	OY 90 GITAGO
Qy 693 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 752	Db 21 ValSer
	150
Qy 753 TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAATCTGGTCTG 812	Db 41 IleAsp
Db 241 PheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeu 260	210
Qy 813 AATGAAGAAATAAACAACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAGGG 872	
	270
Oy 873 GAAAAGCCGTATCATCCCTTTGATCGCAGTCACTTCAAACTGTTCACCATCAAATACGTT 932	81
Db 281 GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal 300	330
Qy 933 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTTAACAGGTAGCGAACGTAAC 992	
	390
Oy 993 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTTCCTACAACAACAACTTC 1052	121
	450
Oy 1053 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1112	141
	510
Qy 1113 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGGACCCGAAGGAGAAAAGCTAGCT	161
Db 361 ThrAsnArgllelleThrValTyrMetGlyLysArgProGluGlyGluAsnAlaSerTyr 380	570
Oy 1173 CATTTAGCT 1181	Db 181 LysAsp
	Qy 630 CTAGCT
	Db 201 LeuAla
US-10-988-943-1 ; Sequence 1, Application US/10988943	Qy 690 GACTCC
0	Db 221 AspSeri
	Cy 750 GAGTTE
TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN	Db 241 GluPhe
FILE REFERENCE: Proteomics CU2003-269	Qy 810 CTGAAT
CURRENT FILING DATE: 2004-11-15; NUMBER OF SEC ID NOS: 61	Db 261 LeuAsn
; SOFTWARE: Patentin Ver. 2.1	Cy 870 GGGGAA
; LENGTH: 415	Db 281 GlyGlu
; ORGANISM: Streptococcus equisimilis US-10-988-943-1	Cy 930 GTTGAT
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Alignment Scores:

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                             AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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             CTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGGAGATAATCACGAT
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; Sequence 252, Application US/10300215
; Publication No. US20030153043A1
; GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
APPLICANT: ADAIR, Fiona Suzanne
APPLICANT: ADAIR, Fiona Suzanne
APPLICANT: CARTER, Graham
: TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
TITLE OF INVENTION: MOWINGER: US/10/300,215
CURRENT APPLICATION NUMBER: US/10/300,215
CURRENT APPLICATION NUMBER: US 09/438,136
FRIOR APPLICATION NUMBER: WO PCT/GB98/01473
PRIOR PILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1997-05-21
PRIOR PILING DATE: 1997-05-21
PRIOR PILING DATE: 1997-05-21
PRIOR PLING DATE: 1997-05-21
PRIOR PILING DATE: 1997-05-21
PRIOR PILING DATE: 1997-05-21
PRIOR PILING DATE: 1997-07-31
PRIOR PILING DATE: 1997-11-28
PRIOR PILING DATE: 1998-04-14
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Percent Similarity:
Best Local Similarity:
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US-10-300-215-252
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Pred. No.:
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Patent No. US20020165129A1

GENERAL INFORMATION:

APPLICANT: Kryetal, Gerald

APPLICANT: Rabkin, Simon W.

TITLE OF INVENTION: Cell Death

TITLE OF INVENTION: Cell Death

FILE REFERENCE: 50216/003004

CURRENT PAPPLICATION NUMBER: US/09/919,703

CURRENT PILING DATE: 2001-07-31

PRIOR FILING DATE: 1999-04-19

PRIOR FILING DATE: 1999-04-19

PRIOR PILING DATE: 1995-12-05

PRIOR APPLICATION NUMBER: US 60/008,233

PRIOR PILING DATE: 1995-12-06

PRIOR PILING DATE: 1995-12-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FREESEQ for Windows Version 4.0
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LENGTH: 413
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|LysAlaLysGlnGluGlnEeuIleAlaAsnValHisSerAsnAspAspTyrPheGluVal 100
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Matches:
Conservative:
Mismatches:
Indels:
     GENERAL INFORMATION

APPLICANT: CARRY, Francis Joseph
APPLICANT: ADAIR, Fiona Suzame
APPLICANT: HAMILTON, Anita Anne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: CARTER, Graham
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
TITLE OF INVENTION: METHOD FOR THE PROPUE
CURRENT APPLICATION NUMBER: US 10/438,136
PRIOR APPLICATION NUMBER: US 09/438,136
PRIOR PRILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: GB 9710480.6
PRIOR PLING DATE: 1997-05-21
PRIOR APPLICATION NUMBER: GB 9710480.6
PRIOR PRILING DATE: 1997-07-31
PRIOR PELING DATE: 1997-07-31
PRIOR PELLING DATE: 1997-11-28
PRIOR PELLING DATE: 1997-11-20
PRIOR APPLICATION NUMBER: GB 970751.4
PRIOR FILING DATE: 1997-11-20
PRIOR APPLICATION NUMBER: US 60/667,235
PRIOR PELLING DATE: 1997-11-202
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FEASTERE FEASTERE FOR WINDOWS VERSION 4.0
SEQ ID NO 253
LENGTH: A14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-940-235-9 (1-1541) x US-10-300-215-253 (1-414)
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, OTHER INFORMATION: Modified strep protein US-10-300-215-253
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ORGANISM: Artificial Sequence
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27 IleAlaGlyTyrGlyTrpLeuProAspArgProProlleAsnAsnSerGlnLeuValVal
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                             GTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGT
                                                                                                                                                                                                                               Sequence 658, Application US/10474792

Publication No. US20040236072A1

GENERAL INFORMATION:

APPLICANT: Olmsted, Stephen

APPLICANT: Zagursky, Robert

APPLICANT: Winter, Lourie

TITLE OF INVENTION: SURPACE PROTEINS OF STREPTOCOCCUS PYOGENES

TITLE OF INVENTION NUMBER: US/10/474,792

CURRENT APPLICATION NUMBER: US/10/474,792

CURRENT FILING DATE: 2003-10-14

SOFTWARE: Patentin version 3.0

SEQ ID NO 658
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ORGANISM: Streptococcus pyogenes
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                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                               US-09-940-235-9 (1-1541) x US-09-919-703-12 (1-413)
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FRATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-12
                                                               1.47e-171
1928.00
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                                                     Alignment Scores:
Pred. No.:
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PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
PROTEIN
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       CLOT-SPECIFIC STREPTOKINASE
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Matches:
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Mismatches:
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Sequence 52, Application US/10144194A

Publication No: US20030215809A1

GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer G

FILE REPERENCE: 3U 103 R1

CURRENT APPLICATION NUMBER: US/10/144,194A

CURRENT FILING DATE: 2002-06-12

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PatentIn version 3.0

SEQ ID NO 52

LENGTH: 463
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREE
TITLE OF INVENTION: PROTEINS POSSESSING ALTI
TITLE OF INVENTION: CHARACTERISTICS AND A PR
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: 08/471,349
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FREISEQ FOR WINDOWS VERSION 4.0
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
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ORGANISM: Homo sapiens
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                                                                                                                                  GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
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Publication No. US20030059921A1
GENERAL INFORMATION:
APPLICANT: Sahni, Girish
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
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155 ArgArgProHis---GluThrGlyGlyTyTMetLeuGluCysValCysLeuGlyAsnGly
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| Publication No. US20040166519A1
| GENERAL INPORMATION:
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/10/741,601
| CURRENT FILING DATE: 2003-12-22
| NUMBER OF SEQ ID NOS: 26415
| SOFTWARE: PSECSEQ for Windows Version 4.0
| SEQ ID NO 354
| LENGTH: 642
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US-10-741-601-354
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Best Local Similarity:
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191 ArgArgProHis---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGly
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Publication No. US20040249144A1
GENERAL INFORMATION:
TAPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer Genes
TITLE REFERENCE: 3U 103 R1
CURRENT FPLICATION NUMBER: US/10/491,566
NUMBER OF SEQ ID NOS: 148
SOFTWARE: Patentin version 3.1
SEQ ID NO 52
                                        Length:
Matches:
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CORGANISM: Homo sapiens
US-10-491-566-52
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US-10-144-194A-52
                           Alignment Scores:
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Sequence 1072, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT PRILING DATE: 2003-12-22
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FRASESQ for Windows Version 4.0
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155 ArgArgProHis---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGly
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Matches:
                     CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 359
LENGTH: 657
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       CURRENT APPLICATION NUMBER: US/10/741,601
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US-10-741-601-359
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ORGANISM: Homo sapiens
US-10-741-600-1072
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                                                                                                                                             Sequence 1066, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPRESENT: CL001499
CURRENT APPLICATION UMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FESTES for Windows Version 4.0
SEQ ID NO 1066
LENGTH: 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCAC 1487
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234 GlnAspThrArgThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsnArgGly 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 ArgArgProHis---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGly
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US-10-741-601-359
US-10-741-601-359
Sequence 359, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
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                                                    1488 ACCICIGIGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGT
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Conservative:
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85.40%
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US-10-741-600-1066
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Best Local Similarity:
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214 ThrCysLeuGlyGluGlySerGlyArglleThrCysThrSerArgAsnArgCysAsnAsp 233
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155 ArgArgProHis---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGly 173
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174 LysGlyGluTrpThrCysLysProIleAlaGluLysCysPheAspHisAlaAlaGlyThr 193
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155 ArgArgProHia---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGly 173
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                                                                                                                                                                                       ---GCTGGTGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 356, Application US/10741601
| Publication No.: US20040166519A1 |
| GENERAL INFORMATION: |
| APPLICANT: CARGILL, Michele et al. |
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/10/741,601 |
| CURRENT PILLING DATE: 2003-12-22 |
| NUMBER OF SEQ ID NOS: 26415 |
| SOOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 356 |
| LENGTH: 984
                                                                                                                                                                                                                                                                                                                                                                                                          1488 ACCTCTGTGCAGACCACATCGAGGGGATCTGGCCCCTTCACCGATGTTCGT 1538
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-10-741-601-356
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13, Appl 4, Appli 7, Appli 260, App 7, Appli

3, Appli

292, App 5, Appli 8, Appli

Sequence:

Run on:

Searched:

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Sequence 2, Application US/10631558
| Sequence 2, Application US/10631558
| Sequence 2, Application No. US2005026059841
| GENERAL INFORMATION:
| APPLICANT: Kumar, Rajesh
| APPLICANT: Roy, Chait
| APPLICANT: Roy, Chait
| APPLICANT: Roy, Chait
| APPLICANT: Roy, Chait
| APPLICANT: Sundaram, Vasudha
| FILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
| FILE REFERENCE: 07064-00902
| CURRENT PILING DATE: 2003-07-31
| PRIOR APPLICATION NUMBER: US/09/940,235
| PRIOR PILING DATE: 1999-12-23
| PRIOR PILING DATE: 1999-12-23
| PRIOR PILING DATE: 1999-12-24
| NUMBER OF SEQ ID NOS: 28
| SOFFWARE: PASESEQ for Windows Version 4.0
| SEQ ID NO 2
| LENTH: DATE: 
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                               US-10-995-561-621

US-10-995-561-623

US-10-995-561-624

US-10-995-561-628

US-10-995-561-628

US-10-995-561-628

US-10-995-561-634

US-11-013-759-3

US-11-013-759-3

US-11-013-759-4

US-11-013-759-4

US-11-013-759-7

US-11-013-759-7

US-11-013-98-7

US-11-013-98-7

US-11-013-98-7

US-11-013-98-7

US-11-013-98-7

US-11-013-98-1

US-11-013-98-1
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Alignment Scores:
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US-10-631-558-2
                                     265.5
262.5
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189.5
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  -MODEL-frame+ n2p. model - DEV-xlp
-Q=/cgn2 1/USPTO spool p/US09940235/runat 27012006_144220_27676/app_query.fasta_1.7708
-Q=/cgn2 1/USPTO spool p/US09940235/runat 27012006_144220_27676/app_query.fasta_1.7708
-Q=/cgn2 1/USPTO spool p/USO9940235/runat SUFFIX:arapbn - MINMATCH=0.1
-LOOPEXT=0 - LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR. SCORE=pct - THR MAX=100
-THR. MIN=0 - ALIGN=15 - MODE=LOCAL - OUTFWT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0
-NAXIENE-200000000 - USRE-US09940235 @CGN 1 1 1 @runat 27012006 144220 27676
-NCPU=6 - LICPU=3 - NO MMAP - LARGEQUERT - NEG $\overline{SCORE}$ = 0 - \overline{MIT} - DSPBECCK=10\overline{OTF}$
-LONGING - DEV TIMEOUT=120 - WARN TIMEOUT=30 - THRRADS=1 - XGAPEXT=0.5
-FGAPOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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1: /cgn2 = 6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

2: /cgn2 = 6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2 = 6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2 = 6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2 = 6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

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8: /cgn2 = 6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                  GenCore version 5.1.6
, Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                              OM nucleic - protein search, using frame_plus_n2p model
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US-11-032-951-12
US-10-631-558-4
US-11-006-119-31
US-10-995-561-622
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US-10-995-561-623
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Database :

1264597860

Result

993 TTAGACTTCACAGATTTATACGATC	Caps   Caps
Pred. No.:   3.246-141   Length:   414	Oy 693 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 752

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TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: UNMABER:
CURRENT APPLICATION NUMBER: 02/09/940,235
FRIOR APPLICATION NUMBER: US/09/940,235
FRIOR PILING DATE: 2002-04-09
FRIOR PILING DATE: 1999-12-23
FRIOR FILING DATE: 1999-12-23
FRIOR FILING DATE: 1999-12-23
FRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 259
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Matches:
Conservative:
Mismatches:
Indels:
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US-11-006-119-31
Sequence 31, Application US/11006119
Publication No. US20050260691A1
GENERAL INFORMATION:
APPLICANT: Mado, Momar
APPLICANT: Caffrey, Rebecca
APPLICANT: Spithil, Terry
APPLICANT: Spithil, Terry
APPLICANT: Podust, Vladimir
APPLICANT: Pedust, Vladimir
APPLICANT: Perichon, Regis
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632.00
87.59%
85.40%
23.27%
       Sundaram, Vasudha
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US-10-631-558-4
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Best Local Similarity:
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Pred. No.:
Score:
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                                                      ATTGATITITGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
                                                                                                                            AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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US-10-611-558-4

Sequence 4, Application US/10631558

Publication No. US20050260598A1

GENERAL INFORMATION:
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
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US-09-940-235-9 (1-1541) x US-10-995-561-622 (1-657)
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LENGTH: 642
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995, 561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASEUSEQ for Windows Version 4.0
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143 LysGlyGluTrpThrCysLysProlleAlaGluLysCysPheAspHisAlaAlaGlyThr
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TITLE OF INVENTION: Serum Biomarkers for Chagas Disease; FILE REFERENCE: 016866-012130US; CURRENT APPLICATION NUMBER: US/11/006,119; CURRENT FILING DATE: 2004-12-06; PRIOR APPLICATION NUMBER: US 60/527,153; PRIOR FILING DATE: 2003-12-05; PRIOR PELICATION NUMBER: US 60/557,093; PRIOR FILING DATE: 2004-04-22; PRIOR FILING DATE: 2004-04-22; PRIOR FILING DATE: 2004-11-06; NUMBER OF SEQ ID NOS: 38; SOPTWARR: PARCHING DATE: 2004-11-06; NUMBER OF SEQ ID NOS: 38; SOPTWARR: PARCHING UP SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: N-terminal 28.7 fragment of Fibronectin
US-11-006-119-31
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Matches:
Conservative:
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Indels:
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632.00
87.59%
85.40%
23.27%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE REPERRENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 622
LENGTH: 657
                                                                                                                                                                                                                                                                                                                                 214 ThrCygLeuGlyGluGlySerGlyArgIleThrCygThrSerArgAsnArgCygAsnAng 233
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Mismatches:
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                                                                                    Length:
Matches:
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85.40%
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632.00
87.59%
85.40%
23.27%
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                    Percent Similarity:
Best Local Similarity:
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Pred. No.:
                                US-10-995-561-631
                                                                  Alignment Scores:
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214 ThrCysLeuGlyGluGlySerGlyArgIleThrCysThrSerArgAsnArgCysAsnAsp 233
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOOIS59
CURRENT PAPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 633
                              194 SerTyrValValGlyGluThrTrpGluLy8ProTyrGlnGlyTrpMetMetValAspCy8
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US-10-995-561-633
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Fublication No. US20050272054A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE REFERENCE: CLOUSES, SET CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING, DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 629
                                                                                                          174 LysGlyGluTrpThrCysLysProileAlaGluLysCysPheAspHisAlaAlaGlyThr
                                                                                                                                                             155 ArgArgProHis---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGly
                                                                         1191 CAGGCGCAA---CAGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACT
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ORGANISM: Homo sapiens
US-10-995-561-629
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Percent Similarity;
Best Local Similarity:
Query Match:
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US-10-995-561-629
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                              US-10-995-561-627
                                                              Alignment Scores:
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   Sequence 623, Application US/10995561

Publication No. U520050272054A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: CENEILC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995, 561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FRALSEQ for Windows Version 4.0

SEQ ID NO 623

LENGTH: 2355
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDILOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 627
LENGTH: 2355
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US-10-995-561-623
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US-10-995-561-623
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| Sequence 1545, Application US/10821234|
| Sequence 1545, Application US/10821234|
| Sequence 1545, Application WS-10820050255114A1|
| GENERAL INFORMATION:
| APPLICANT: Labat, Ivan |
| APPLICANT: Adammani, Susan |
| APPLICANT: Tang, Y. Tom |
| TITLE OF INVARITON: Methods for Diagnosis and Treatment of Preeclampsia |
| FILE REFERENCE: 821A |
| CURRENT APPLICATION NUMBER: US/10/821,234 |
| CURRENT FILING DATE: 2004-04-07 |
| PRIOR APPLICATION NUMBER: US 60/462,047 |
| PRIOR APPLICATION NUMBER: US 60/462,047 |
| PRIOR PILING DATE: 2003-04-07 |
| SEQ ID NOS: 1704 |
| SOFTWARE: PLE SEQ_Genes Version 1.0 |
| SEQ ID NO 1545 |
| LENGTH: 2384
                                                                                                                                                                                                                                                                                           1143 AAGCGACCCGAAGGAGAGAATGCTAGCTACCATTTA------GCTGGTGGTGGTGGC
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Conservative:
Mismatches:
Indels:
Gaps:
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87.59%
85.40%
23.27%
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AACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCAC 1487
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Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: US/10/995,561

CURRENT PILITIG DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 621
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866 ServalTyralaLeuLysAspThrLeuThrSerArgProAlaGlnGlyvalValThrThr 885
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------AlaThrGluThrThrIleThrIle---
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886 LeuGluAsnValSerProProArgArgAlaArgValThrAsp------
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Publication No., US20050272054A1
GENERAL INFORMATION.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILLING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRAEESQ for Windows Version 4.0
SEQ ID NO 626
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155 ArgAroHis---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnĠly 173
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203 LysGlyGluTrpThrCysLysProIleAlaGluLysCysPheAspHisAlaAlaGlyThr
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOPTWARE: FastSeQ for Windows Version 4.0
SEQ ID NO 632
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|SerValTyrAlaLeuLysAspThrLeuThrSerArgProAlaGlnGlyValValThrThr 173
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205 ThrGlyPheGlnValAspAla------ValProAlaAsnGlyGlnThrProIleGln
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609	ACCATCACATCTCAAGAATTACTAGCTCAAGCA	
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699	9GGCTATACGATTTATGAACGTGACTCTCAATCGTCACTCATGACAAT 716	
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840	) ATCTCTGAGAAATATTACGTCCTTAAAAAGGG	
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1003	ß GlnProSerValGlyGlnGlnMetIlePheGluGluHisGlyPheArgArgThrThrPro 1022	
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1023	:::           :::   ProThrThrAlaThrProlleArgHisArgProArgProTyrProProAsnValGlyGln 1042	
006	AGTCACTTGAAACTGTTCACCATCAAATACGTTGATGTCGATACCAAATTGCTA 956	
1043		
957	7 AAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAACTTTAGACTTTATACGAT 1016	
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1017	) CCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTTGGTATTATGGACTAT 1076	
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1087	ThrieuThrdiyLeuThrArgGlyAlaThrTyrAsnIleIleValGluAlaLeuLysAsp 1106	
1095	GAGGATAATCACGATGACACCAACCGTATCATAACCGTTTATATATGGGCAAGCGACCCGAA 115	
1107	GINGINATGHISLYSVALArgGIUGIUVALVALTNINAGIJASNSErVALASNGIU	
1126	Carandariacidaciaccallinacidacidacidaccadaccacacacacacacacacacac	
1215	GCTGAGAAGTGTTTTGATCATGCTGCTGGACTTCCTATGTGGTCGGAGAAACGTGGGAG 127	
1132	:::            AspAspSerCysPhcAspProTyrThrValSerHisTyrAlaValdlyAspGluTrpGlu	
1275	AAGCCCTACCAAGGCTGGATGATGGATGGATGCCTGGGGGAGAGGGGGGGG	
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1335	ATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACGAAGGACATCCTATAGAATT 139	
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Search completed: January 28, 2006, 02:57:30 Job time : 25.4619 sec8

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streptokinase precursor - Streptococcus "equisimilis"

()Species: Streptococcus "equisimilis"

C)Accession: A22801

C)Accession: A22801

R)Malke, H.; Roe, B.; Ferretti, J.J.

Gene 34, 357-362, 1985

A;Title: Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H.
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A;Molecule type: DNA
A;Residues: 1-440 <MAL>
A;Cross-references: UNIPROT:P00779; UNIPARC:UPI000002BE73; GB:X72832; NID:g407876; PIDN
C;Genetics:
fibronectin - Afri
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Ggn2 1/USFTO spool py/USO9940235/runat 27012006 144218 27578/app_query.fasta_1.7708
-Q=/Ggn2 1/USFTO spool py/USO9940235/runat 27012006 144218 27578/app_query.fasta_1.7708
-DB=FIR -QFRT=fastan -SUPFIX=rpr -MINMATCH=0.1 -LOÖPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -EMD=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWH=PAPP.TSCORE=500 -MINIEN=0 -MAXIEN=200000000
-USER=USO9940235_@GGN 1 1 185 @runat 27012006 144218 27578 -NCQU=6 -LCPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-NO THREOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Copyright (c) 1993 - 2006 Compugen Ltd.
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streptokinase (EC 3.4.-.-) - Streptococcus sp.
C;Species: Streptococcus sp.
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C;Species: Streptococcus sp.
C;Accession: A00967
B;Jackson, K.W.; Tang, J.
Biochemistry 21, 6620-6625, 1982
A;Title: Complete amino acid sequence of streptokinase and its homology with serine prot A;Reference number: A00967; MuID:83127125; PMID:6760891
A;Accession: A00967
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Bb 247  Oy 753  Bb 267  Oy 813  Bb 287  Oy 813  Oy 873  Oy 933	Db   327 AspValAsnThrAsnGluLeuLysSerGluGlnLeuLeuThrAlaSerGluGlyAsn 346	### PRESENT 5 ### JU0292 ### Streptococcus pyogenes ### Cipecters Cipecters Pyogenes ### Cipecters Cipecters Pyogenes ### Cipecters Cipecters Pyogenes ### Cipecters Cipecters Cipecters ### Cipecters Cipecters Cipecters ### Cipecters
streptokinase A precursor - Streptococcus pyogenes (strain SF130/13) C;Species: Streptococcus pyogenes C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004 C;Cocession: S02724 R;Walter; F; Siegel, M; Malke, H R;Walter; F; Siegel, M; Mill: 89160264; PMID: 2646590 A;Reference number: S02724 A;Residues: 1-440 < WAL> A;Residues: 1-440 < WAL> A;Residues: 1-440 < WAL> A;Residues: 1-440 < WAL> A;Cocesion: S6A A;Coces-references: UNIPROT: P10520; UNIPARC: UP1000017021D; EMBL:X13399; NID: 947435; C;Genetics: A;Gene: Ska C;Superfamily: streptokinase C;Superfamily: streptokinase #status predicted < MAI> F;27-440/Product: streptokinase #status predicted < MAI>	Alignment Scores:  Pred. No.:  2.21e-113  Length: 440  Score:  1779.00  Matches: 338  Score:  1779.00  Matches: 338  Conservative: 21  Best Local Similarity: 81.24  Query Match: 24  Indeals: 0  Gaps: 0  Gaps: 0  US-09-940-235-9 (1-1541) x S02724 (1-440)  Oy 33 ATAGCTGCTCTGAATGCTACTAGATCTTCTGTAAATAACAGCCAATTGGTTGT  OY 33 ATAGCTGCTCTGAATGCTACTAGATCTTCTGTAAATAACAGCCAATTGGTTGT  OY 34 ATAGCTGTCTGAAGGCGAATTGATTTTTTAAATATTTTTTAAAATC 152  OY 93 AGCGTTGCTGGTACTGAGGCGAAATCAGACATTAGTCTTAAAATCTTTTTTAAAATC 152  OY 93 AGCGTTGCTGGTACTGTAGGCGGAATCAGACATTAGTCTTTAAATCTTTTTAAAATC 152  OY 93 AGCGTTGCTGGTACTGTAGGCGGAATCAGACATTAGTCTTTAAATCTTTTTAAAATC 152  OY 93 AGCGTTGCTGGTACTGTAGGCGGAATCAGACATTAGTCTTTAAATCTTTTTAAAATC 152  OA 93 AGCGTTGCTGGTACTGTAGGCGGAATCAAGACATTAGTCTTTAAATCTTTTTTAAAATC 152  OA 93 AGCGTTGCTGGTACTGTAGGCGGAATCAAGACATTAGTCTTTAAATCTTTTTTAAAATC 152  OA 93 AGCGTTGCTGGTACTTAAAATCTTTTTTTAAAATCTTTTTTAAAATCTTTTTT	GATGTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGAAGACCTAAATCA AspLeuThrSerGlnProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer AAACCATTGCTACTGATGGCGCGAAGGCAAGACCTTAACTACTA LysProPheAlaThrAspAsnGlyAlaMetProHisLysLeuGluLysAlaAspLeuLeu AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTAACTTCAAGGTC L

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streptokinase A precursor - Streptococcus pyogenes (strain NZ131)

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C;Species: Streptococcus pyogenes
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S04168
R;Huang, T.T.; Malke, H.; Ferretti, J.J.
Mol. Microbiol. 3, 197-205, 1989
A;Title: The streptokinase gene of group A streptococci: cloning, expression in Escheri A;Reference number: S04168; MUID:89343623; PMID:2668686
A;Reference number: S04168
A;Molecule type: DNA
A;Residues: 1-440 <HUA>
A;Cross-references: UNIPROT:Q57391; UNIPARC:UPI00000BD04A; EMBL:X51517; NID:g47437; PID
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Indels:
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C,Superfamily: streptokinase
F,1-26/Domain: signal sequence #status predicted <SI
F,27-440/Product: streptokinase A #status predicted
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		114	Oy 1113 ACCAACCGTATCATAACCGTATTATATCGCCAACCGAACGACAATGCT 1166
Db   247 SerSerIleValThrHisAepAsenAepIlePheArgThrIleLeuProMetAepGlnGlu 266   753 TTTACTTACCGTGTAAAAATCCGGTCTC 812   1	C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004 C;Accession: S53334 B;Shi, G.Y.; Chang, B.I.; Chen, S.M.; Wu, D.H.; Wu, H.L. B;Ochem. J. 304, 235-241, 1994 A;Title: Function of streptokinase fragments in plasminogen activation. A;Reterence number: S53334 A;Recession: S53334 A;Accession: S53334 A;Accession: Speliminary A;Molcoule type: protein A;Residues: 1-197 <shi: a;cross-references:="" td="" uniparc:upi000017ac2c<="" uniprot:q7m115;=""><td>Alignment Scores: 8.69e-38 Length: 197  Score: 667.00 Matches: 167  Percent Similarity: 44.71% Conservative: 2  Query Match: 24.56% Indels: 208  DB: 24.56% Gaps: 9</td><td>TACTGATGCTRATGCTRC                                    </td></shi:>	Alignment Scores: 8.69e-38 Length: 197  Score: 667.00 Matches: 167  Percent Similarity: 44.71% Conservative: 2  Query Match: 24.56% Indels: 208  DB: 24.56% Gaps: 9	TACTGATGCTRATGCTRC

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A;Accession: A22245
A;Molecule type: mRNA
A;Residues: 1948-2067 <UME>
A;Cross-references: UNIPARC:UPI00000046A; GB:M27589; NID:G182705; PIDN:AAA52465.1; PID
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A; Residues: 1975-1991;2017-2039 <UM2>
A; Residues: 1975-1991;2017-2018
A; Sekiguchi, K.; Klos, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A; Title: Human liver fibronectin complementary DNAs: identification of two different mental precession: 156273
A; Reference number: 152394; MUID:87026578; PMID:3021206
A; Accession: 165273
A; Residues: 1979-1990, 2016-2018, NY, 2020-2081, 2113-2127 <SEK>
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A,Residues: 32-47,'C',49-51,'S',53-72,'A',74-290 <GAR1>
A,Cross-references: UNIPARC:UPI0000174335
R,Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A;Title: Further characterization of the binding of fibronectin to gelatin reveals the jA:Reference number: S34791; MUID:93312001; PMID:8323285
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A,Title: The cell attachment domain of fibronectin. Determination of the primary structu
A,Reference number: A92386, MUID:82265604; PMID:7050098
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A;Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa don
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A; Residues: 291-300,551-560 <GAR2>
A; Cross-references: UNIPARC:UPI0000174336; UNIPARC:UPI0000174337
R; Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A; Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A; Reference number: A60904; MUID:87019725; PMID:3532418
                                                                                       FBBS Lett. 186, 31-34, 1985
A;Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A;Reference number: A22245; MUID:85231203; PMID:2989004
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A; fitle: Primary structure of a DNA- and heparin-binding domain (domain III) ir A; Reference number: A23901, MUID:86008277; PMID:3900070
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J. Biol. Chem. 257, 9593-9597, 1982
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A;Residues: 1441-1548 <-PIE>
A;Cross-references: UNIPARC:UPI0000141CD5
A;Note: residues 1524-1527 are responsible for the cell-binding activity
R;Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
                                 R; Umezawa, K.; Kornblihtt, A.R.; Baralle, F.E.
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A;Residues: 616-677,'Q',679-703,'PT' <CAL>
A;Cross-references: UNIPARC:UP10000174339
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A;Residues: 293-301 <GRI>
A;Cross-references: UNIPARC:UP10000174338
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                                                     A; Modecule type: DNA
A; Residues: 1-49 < CBA>
A; Cossarion: Az2646
A; Modecule type: DNA
A; Residues: UNIPROT: P02751; UNIPROT: Q14327; UNIPARC: UPI000016A926; GB: M15801; NI
R; Oldberg, A.; Ruoslahti, B.
J; Biol. Chem. 261, 2113-2116, 1986
A; Title: Evolution of the fibronectin gene.
A; Reference number: A26284; MUID: 86111901; PMID: 3003095
A; Residues: 1447-1540 < CLD
A; Residues: 1447-1540 < CLD
A; Residues: 1447-1540 < CLD
A; Residues: 1494 as Glu
B; Residues: 16, 3545-3557, 1988
A; Reference number: S00848; MUID: 88233940; PMID: 3375063
A; Residues: 1594-1767, 'V', 1769-1783 < PAO>
A; Residues: 1594-1767, 'V', 1769-1783 < PAO>
A; Ross-references: UNIPARC: UPI000017432B; EMBL: X0771B; NID: 931402
A; Note: the authors translated the codon AAC for residue 1631 as Asp
B; Nibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
BEBS Lett. 207, 287-291, 1986
A; Hell Codon AAC for residue 1631 as Asp
B; Nibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
A; Note: the authors translated the codon AAC for residue 1631 as Asp
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A.Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:
A.Reference number: A24854
A.Molecule type: DNA
A.Residues: 1992-2147 (VIBS)
A.Residues: 1992-2147 (VIBS)
A.Residues: 1992-2147 (VIBS)
A.Residues: 1992-2147 (VIBS)
A.Residues: 1992-2145 (VIBS)
A.Residues: 1992-2145 (VIBS)
A.Residues: DNA
A.Residues: DNA
A.Residues: A24476
A.Title: Human fibronectin is synthesized as a pre-propolypeptide.
A.Residues number: A24476
A.Residues: not compared with conceptual translation
A.Residues: 114, 70' .16-38 (GUT>
A.Residues: 114, 70' .16-38 (GUT>
A.Residues: 114, 70' .16-38 (GUT>
A.Residues: 12-159, 1985
A.Title: Primary structure of human fibronectin: differential splicing may generate at 1
A.Residues: nucleic acid sequence not shown
A.Residues: 13-1344, 1346-2080; 2112-2386 «ROR>
A.Residues: 32-1344, 1346-2080; 2112-2386 «ROR>
A.Residues: 22-1344, 1346-2080; 2112-2386 «ROR>
A.Residues: 23-1344, 1346-2080; 2112-2386 «ROR>
A.Residues: 12-1344, 1346-2080; 2112-2386 «ROR>
A.Reterence number: AB1008; MUID:84272258; PMID:6462919
A.Reference number: A93529; MUID:84272258; PMID:6462919
A.Reference number: A93529; MUID:84272258; PMID:6462919
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A;Cross-references: UNIPARC:UP1000016A928; GB:M10905; NID:G182696; PIDN:AAA52462.1; PID:
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A,Reference number: A90495, MUID:85280409, PMID:2992573
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R;Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
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R;Oldberg, A.; Linney, B.; Ruoslahti, E.
D siol. Chem. 258, 10193-10195, 1983
A;Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell
A;Reference number: A21011; MUID:83290929; PMID:6688418
Reference number: A26460; MUID:87175578; PMID:3031656
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A; Residues: 973-2080;2112-2386 <KO2>
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A; Residues: 1594-2386
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C;Species: Streptococcus pyogenes
C;Date: 24-Uul-1998 #sequence_revision 24-Jul-1998 #text_change 22-Jun-1999
C;Date: 24-Uul-1998 #sequence_revision 24-Jul-1998 #text_change 22-Jun-1999
C;Accession: 877671; 877672; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671; 877671;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPARC:UPI000000562; EMBL:U25853; NID:g818908; PIDN:AAA85729.1; PI
A;Experimental source: strain ET1/M1
A;Note: allele 2
A;Accession: S77672
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A;Molecule type: DNA
A;Residues: 1-128 <KA2-
A;Cross-references: UNIPARC:UP10000000562; EMBL:U25854; NID:g818910; PIDN:AAA85730.1; PI
A;Experimental source: strain E2/M3
A;Note: allele 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               streptokinase A (EC 3.4...) (alleles 2 and 3) - Streptococcus pyogenes (fragment)
                                                                                                                                                                                              AACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAAGTGTGAGAGGGCAC 1487
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                                                                                                                                                                                                                                      CAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGA
                                                                                   GlnAspThrArgThrSerTyrArg1leGlyAspThrTrpSerLysLysAspAsnArgGly
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                                                                                                                                                                                                                                                                                                                                         C; Keywords: hydrolase; plasminogen activator; virulence
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A;Cross-references: GDB:119135; OMIM:135600
A;Gene: GDB:FN1
A;Cross-references: GDB:119135; OMIM:135600
A;Gene: GDB:PN1
A;Cross-references: GDB:119135; OMIM:135600
A;Map position: 264-264
A;Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C;Superfamily: fibronectin type I repeat homology; fibronectin type II repeat homology;
C;Keywords: acute phase; alternative splcidical cslc
F;2-26/Domain: signal sequence #status predicted cslc
F;2-27/Domain: propeptide #status predicted cslc
F;2-272/Domain: fibronectin #status experimental cMAT>
F;52-272/Domain: fibronectin type I repeat homology clF2>
F;141-179/Domain: fibronectin type I repeat homology clF3>
F;141-179/Domain: fibronectin type I repeat homology clF3>
F;166-225/Domain: fibronectin type I repeat homology clF5>
F;308-342/Domain: fibronectin type I repeat homology clF5>
F;308-342/Domain: fibronectin type II repeat homology clF6>
F;308-355/Domain: fibronectin type II repeat homology clF6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: A23891
A,Molecule type: protein
A,Rolecidues: 2071-2080,2112-2356 <GAR4>
A,Cross-references: UNIPARC:UPI000017433C; UNIPARC:UPI000017433D
C,Comment: The extra domain and connecting strand 3 are subject to developmental and tis
C;Comment: The callular and plasma fibronectins are high molecular weight glycoproteins, at transformation.
                           A,Accession: A32517
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: brotein
A;Residues: 1589-1630, '1,1722-2058 cGAR3>
A;Cross-references: UNIVPARC:UPI000017433A
B;Cross-references: UNIVPARC:UPI000017433A
R;Tressel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pand Biochem. J. 274, 731-738, 1991
A;Title: Human plasma fibronectin. Demonstration of structural differences between the A;Reference number: S14357; MUID:91190085; PMID:2012601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIGCCIGGGAGAAGGCAGCGCACCATCACTIGCACTICTAGAAATAGAIGCAACGAT
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                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: protein
A;Residues: 1614-1630, "17,1722-2081,2113-2244 <TRE>
A;Resos-references: UNIPARC:UPI000017438
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
D, Biol. Chem. 260, 10320-10325, 1985
A;Title: Primary structure of human plasma fibronectin.
A;Reference number: A23891; MUID:85261459; PMID:4019516
A;Reference number: A32517; MUID:87241275; PMID:3593230
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Matches:
Conservative:
Mismatches:
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F;1970-1972/Region: cell attachment (R-G-D) motif
F;1970-1972/Region: cell attachment (R-G-D) motif
F;1982-2062/Domain: fibronectin type III repeat homology <FN30>
F;1985-216/Domain: fibronectin type II repeat homology <FR10>
F;2085-2124/Domain: fibronectin type I repeat homology <1F10>
F;2104-2109/Domain: fibronectin type I repeat homology <1F11>
F;2104-2109/Domain: fibronectin type I repeat homology <1F11>
F;2174-2209/Domain: fibronectin type I repeat homology <1F11>
F;1714-2209/Domain: fibronectin type I repeat homology <1F11>
F;1714-2209/Domain: fibronectin type I repeat homology <1F11>
F;1714-2209/Domain: fibronectin type I repeat homology <1F10>
F;1714-2209/Domain: fibronectin type I repeat homology <1F10-229,227-239,277-304,302-
F;1745-2167,2174-2200,2198-2209/Disulfide bonds: fistatus predicted
F;1895,1947,1914/Binding site: carbohydrate (Asn) (covalent) #status spent
F;1894/Binding site: carbohydrate (Thr) (covalent) #status sperimental
F;2246/Disulfide bonds: interchain (to 2250) #status predicted
F;2250/Disulfide bonds: interchain (to 2246) #status predicted
F;2250/Disulfide bonds: interchain (to 2246) #status specimental
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submitted to the EMBL Data Library, July 1989
A.Reference number: 814428
A.Accession: 814428
A.Accession: 814428
A.Residues: 1-2477 cHYN>
A.Cross-references: UNIPROT: P04937; UNIPARC: UPI000012A7C6; EMBL: X15906; NID: 956163; PIDM A.Residues: 1-2477 cHYN>
A.Cross-references: UNIPROT: P04937; UNIPARC: UPI000012A7C6; EMBL: X15906; NID: 956163; PIDM A.Residues: J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A.Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript. A.Reference number: 812455; MUID: 88054951; PMID: 2445560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 ThrCysLeuGlyGluGlySerGlyArgIleThrCysThrSerArgAsnArgCysAsnAsp 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 ABnLeuleuGlnCysIleCysThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHis 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1143 AAGCGACCCGAAGGAGAATGCTAGCTACCATTTA------GCTGGTGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 LysGlyGluTrpThrCysLysProlleAlaGluLysCysPheAspGlnAlaAlaGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTATGTGGTCGGAGAACGTGGGAGAGCCCTACCAAGGCTGGATGATGGTTGT
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Conservative:
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Conferce 13 Design Sangement evention 11-Dec-1988 fleet. Change 09-Jul-2004
Concession: Aded52; Bus Detaile Sanders evention 11-Dec-1988 fleet. Change 09-Jul-2004
Concession: Aded52; Business Sanders Sander
F;1600-1682/Domain: fibronectin type III repeat homology F;1692-1773/Domain: fibronectin type III repeat homology
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|21 LysGluLysThrAsnAsnThrAsp 128
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P;1356-1439/Domain: fibronectin type III repeat homology <FN31>
P;1447-1529/Domain: fibronectin type III repeat homology <FN3J>
P;1537-1619/Domain: fibronectin type III repeat homology <FN3J>
P;1537-1619/Domain: fibronectin type III repeat homology <FN3I>
F;1631-1713/Domain: fibronectin type III repeat homology <FN3I>
F;1631-1893/Domain: fibronectin type III repeat homology <FN3I>
F;1801-1894/Domain: fibronectin type III repeat homology <FN3I>
F;1912-2074/Domain: fibronectin type III repeat homology <FN3I>
F;2181-2183/Region: cell attachment (R-G-D) motif
F;2181-2335/Domain: fibronectin type III repeat homology <FN3I>
F;2181-2335/Domain: fibronectin type III repeat homology <FN3I>
F;2181-2335/Domain: fibronectin type II repeat homology <FN3I>
F;2385-2420/Domain: fibronectin type I repeat homology <FRIP>
F;2385-2420/Domain: fibronectin type I repeat homology <FRIPONECTIN (FRIPONECTIN (FRIPO
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C;Species: Streptococcus pyogenes
C;Species: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S77680
R;Kapur, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser, Mol. Microbiol. 16, 509-519, 1995
A;Title: Molecular population genetic analysis of the streptokinase gene of Streptococcus, A;Reference number: S77671; MUD:96037795; PMID:7565111
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A; Accession: 159049
A; Accession: 1722-180A
A; Accession: 1722-180A
A; Accession: 1722-180A
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A,Residues: 2052-2237 <FAM>
A,Falkenberg, C.; Enghild, J.J.; Thogersen, I.B.; Salvesen, G.; Akerstroem, B.
Biochem. J. 301, 745-751, 1994
A,Fitle: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in A,Reference number: S46203; MUID:94330948; PMID:7519849
A,Recession: S46203
A,Status: preliminary
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A,Residues: 1-139,2382-2477 <PAT>
A,Cross-references: UNIPARC:UPI000017095C; UNIPARC:UPI0000177AEF; EMBL:X05831
A,Fore: the authors translated the codon CCT for residues 51 and 94 as Ala
R,Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
A,421-431, 1983
A,71tle: Three different fibronectin mRNAs arise by alternative splicing within the codi
A,Reference number: A27252; MUID:84082067; PMID:6317187
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A; Residues: 1183-1192; GLN', 1268,'P',1270-1271,'D',1273,'CF',1276,'PY',1385-1399 < PAL>
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A; Cross-references: UNIPARC:UPI0000177AEC; UNIPARC:UPI0000177AED; UNIPARC:UPI0000177AEB
B; B; A; Commanization C; Schwarzbauer, J.E.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1987
EMBO J. 6, 2565-257
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A;Molecule type: mRNA
A;Rosedues: 1586-1720, "T'.1722,1813-2477 <SC2>
A;Croserreferences: UNIPARC:UPI0000177AF0
R;Odermatt, E.; Tamkun, J.W.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A;Title: Repeating modular structure of the fibronectin gene: Relationship to protein a, Reference number: 159049; MUID:86016741; PMID:3863113
                                                                                                                                                                                                                                                                      R,Tamkun, J.W.; Schwarzbauer, J.B.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A,Title. A single rat fibromectin gene generates three different mRNAs by alternative A;Reference number: A22319; MUID:84298097; PMID:6089177
                                                          A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 609-1810, 'T, 1812-2283 <SCH>
A;Cross-references: UNIPARC:UF10000177AEA; EMBL:X15906
R;Tamkun, J.W.; Schwarzbauer, J.B.; Hynes, R.O.
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Claccesion: 877679

Rikapur, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser, M.; Microbiol. 16, 509-519, 1995

A;Title: Molecular population genetic analysis of the streptokinase gene of Streptococco A;Reference number: 877671; MUID:96037795; PMID:7565111

A;Accession: 877679

A;Accession: 877679

A;Molecule type: DNA

A;Residues: translation not shown

A;Residues: 1-128 cKAP>
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                                      513 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
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C;Keywords: hydrolase; plasminogen activator; virulence
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C; Species: Streptococcus pyogenes
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C; Accession: S77688
R; Kapur, V. Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser, Mol. Microbiol. 16, 509-519, 1995
A; Title: Molecular population genetic analysis of the streptokinase gene of Streptococcu A; Receive number: S77671; MUID: 96037795; PMID: 7565111
A; Accession: S7768
A; Status: translation not shown
A; Residues: 1-128 cKAP>
A; Cross-references: UNIPROT: Q54695; UNIPARC: UP100000BDBDC; EMBL: U25870; NID: 9818942; PIC
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C; Superfamily: streptokinase
C; Keywords: hydrolase; plasminogen activator; virulence
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C,Superfamily: streptokinase
C,Keywords: hydrolase; plasminogen activator; virulence
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A.Fatus: nucleate and sequence on the sequence of the sequence of the sequence (NCEPF) 74733
A.Gross-references: UNIPARC.[PF10000177AE7; GB:W77820
A.Note: sequence extracted from NCED the pack homology; fibronectin type I repeat homology of PT>
C.Superfamily: fibronectin: fibronectin type I repeat homology of PT>
F.100-138/Domain: fibronectin type I repeat homology of PT>
F.100-138/Domain: fibronectin type I repeat homology of PT>
F.1412A.727/Domain: fibronectin type I repeat homology of PT>
F.142A.737/Domain: fibronectin type I repeat homology of PT>
F.142A.737/Domain: fibronectin type I repeat homology of PT>
F.14142A.737/Domain: fibronectin type I repeat homology of PT>
F.150-342/Domain: fibronectin type I repeat homology of PT>
F.150-343/Domain: fibronectin type I repeat homology of PT>
F.151-462/Domain: fibronectin type I repeat homology of PT>
F.151-462/Domain: fibronectin type I repeat homology of PT>
F.151-65/Domain: fibronectin type II repeat homology of PT>
F.151-55/Domain: fibronectin type III repeat homology of PT>
F.151-55/Domain: fibronectin type III repeat homology of PT>
F.151-55/Domain: fibronectin type III repeat homology of PT>
F.161-63/Domain: fibronectin type III repeat homology of PT>
F.165-107/Domain: fibronectin type III repeat homology of PT>
F.166-108/Domain: fibronectin type III repeat homology of PT>
F.161-108/Domain: fibronectin type III repeat homology 
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(ibronectin - African clawed frog
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(ibronectin - A43908 #sequence_revision 31-bec-1993 #text_change 12-Feb-1999
(ibronectin A43908 #sequence_revision 31-bec-1993 #text_change 12-Feb-1999
(ibronectin A43908 #sequence not alternatively spliced fibronectin mRNAs A;Reference number: A43908; MUID:92111942; PMID:1730390
A;Reference number: A43908
A;Status: nucleic_acid sequence not shown; not compared with conceptual translation
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2373,2371-2383,2390-2416,2414-2425/Disulfide bonds: #status predicted
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TTTACTTACGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG
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F;2463/Disulfide bonds: interchain (to 2459) #status predicted
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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-I- FUNCTION: This protein is not a protease, but it activates plasminogen by complexing with it. As a potential virulence factor, it is thought to prevent the formation of effective fibrin barriers around the site of infection, thereby contributing to the invasiveness of the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-83127125; PubMed-6760891;
Jackson K.W., Tang J.;
TCOmplete amino acid sequence of streptokinase and its homology with
serine proteases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=85232082; PubMed=2989113; DOI=10.1016/0378-1119(85)90145-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malke H., Roe B.A., Ferretti J.C.;
"Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A.";
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Q7x084
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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(Rel. 47, Last annotation update)
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NCBI_TaxID=119602;
STRAIN=H46A;
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10-MAY-2005
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Command line parameters:

**ODEL=frame+ n.2p model - DEV=Xlp
-Q=/Cgn12_1/USFDQ_pmodel - DEV=Xlp
-Q=/Cgn12_1/USFDQ_pmodel - DEV=Xlp
-Q=/Cgn12_1/USFDQ_pmodel - DEV=Xlp
-Q=/Cgn12_1/USFDQ_pmodel - DEV=Xlp
-QEMT_efastan - SUFFIX=Lup - MINNATCH=0.1 - LOOPCI=0 - LOOPEXT=0
-DB=UniProt - QEMT_efastan - SUFFIX=Lup - MINNATCH=0.1 - LOOPCI=0 - LOOPEXT=0
-UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-DOCALIGN=200 - THR_SCORE=pct - THR_NATEL = 100 - THR_NI=0 - AALIGN=15. MODE=LOCAL
-OUTFWT=ptc - NORM=EAX - HEAPSIZE=500 - MINIENS - AALIGN=15. MODE=LOCAL
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P10520
Q532x6
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Q7x0y3
Q7x0y3
Q7x0y3
          GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                  protein search, using frame_plus_n2p model
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                                                                          AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
NCBI_TaxID=119602;
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R PIR; AZ2832; CAA51351.1; -; Genomic_DNA.
R PIR; A22801; BZSO.
R PDB; 1BML; X-ray; BZSO.
R PDB; 1BML; X-ray; B=40-173.
R PDB; 1L4Z; X-ray; B=27-773.
R PDB; 1L4Z; X-ray; B=40-173.
R PRINTS; PRO1753; STREPKINASE.
W BYINTS; PRO1753; STREPKINASE.
W SIGNAL, Virulence.
T SIGNAL
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                                          AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTA CGTCCTTAAAAAAGG
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COSTA C.S., TOTTES F.A.G., Filho S.A.;
SUBMILGE (AUG-2003) to the EMBL/GenBank/DDBJ databases.
SUBL; AY368335, AAQ73571.1; -; Genomic_DNA.
SNR; QGUK57; 59-394.
QG) GO:0016301; F:kinase activity; IEA.
QG; GO:0008243; F:plasminogen activator activity; IEA.
GG; GO:0008243; F:protein binding; IEA.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR0040912; Streptokinase.
FEam; PF02821; Staphylokinase; 3.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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QGUK57_STREQ PRELIMINARY; PRT; 436 AA.
QGUK57;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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NCBI_TaxID=119602;
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          Estrada M.P., Hernandez L., Perez A., Rodriguez P., Serrano R.,
A Rubiera R., Pedraza A., Padron G., Antuch W., la Fuente J., et al.;
T "High level expression of streptokinase in Escherichia coli.";
Biotechnology 0:1138-1142(1992).
R EMBL; S46536; AAC60418.1; Genomic_DNA.
R PDB; 1C4P; X-ray; A/B/C/D=149-285.
R SMR; O53284; 12-372.
R GO; GO:0008243; F:plasminogen activator activity; IEA.
R GO; GO:0005515; F:protein binding; IEA.
R InterPro; IPR008124; Streptokinase.
R InterPro; IPR008124; Streptokinase.
R Pfam; PF02821; Staphylokinase; 3.
R Pfam; PF02821; Staphylokinase; 3.
R RINTS; PR0175; REAPENASE.
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01-JUL-1989 (Rel. 11, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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HSSP. P00779; 1QQR.
SMR; P10619; 63-398.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR00414; Streptokinase.
Pfam; PF02821; Staphylokinase.
PRINTS; PR01753; STREPKINASE.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its the as long as its content is in no way modified and this statement is not GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGAAGGCTTAAGTCCAAAATCA 212 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC 152 fibrin to the Streptococcus.";
Nucleic Acids Res. 17:1262-1262 [1989].

-!- FUNCTION: This proces in not a protease, but it activates plasminogen by complexing with it. As a potential virulence factor, it is thought to prevent the formation of effective barriers around the site of infection, thereby contributing invasiveness of the cells. [1]

NUCLEOTIDE SEQUENCE [GENOMIC DNA].

MEDLINE=89160265; PubMed=292269;

Walter F., Siegel M., Malke H.;

"Nucleotide sequence of the streptokinase gene from a group-G Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, Streptococcus. Streptokinase G. 5521F8825FE1B6EA CRC64; Length:
Matches:
Conservative:
Mismatches:
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J. Bacteriol. 186:110-121(2004).

EMBL; AY234137; AAP39957.1; -; Genomic_DNA.

RSP; Q53284; IC4P.

RSP; Q53284; IC4P.

ROYOVI, 63-398

GO; GO:0008243; F:plasminogen activity; IEA.

GO; GO:0008243; F:plasminogen activity; IEA.

GO; GO:000515; F:protein binding; IEA.

RO; GO:0005124; Straphylokinase.

InterPro; IPR000124; Straphylokinase.

Pfam; PF02821; Staphylokinase; Straphylokinase.

R PRINTS; PR01753; STREPKINASE.
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PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;
Kalia A., Bessen D.B.;
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                                                                              Bacteria; Firmicutes; Lactobacillales;
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"Natural selection and evolution of streptococcal virulence genes
involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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EMBL; AY234129; AAP39949.1; -; Genomic_DNA.

HSSP; Q53284; LQ49.

SMR; Q7X0YB; 63-398.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0008243; F:plasminogen activator activity; IEA.

GO; GO:0005515; F:protein binding; IEA.
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InterPro; IPR004093; Staphylokinase.
InterPro; IPR008124; Streptokinase.
Pfam; PF02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
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                                                                                                  STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Makagawa I., Kurokawa K., Yamaashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of am M3 strain of Streptococcus pyogenes reveals a large-scale genomic rearrangement in invasive strains and new insights into phage evolution.";
                                                                               GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                         307 GluSerProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal
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STRAIN=MGAS315 / Serotype M3;
MEDLINE=2213808; PubMed=1212206; DOI=10.1073/pnas.152298499;
MEDLINE=2213808; PubMed=1212206; DOI=10.1073/pnas.152298499;
MEBERES S.B., Sylva G.L., Baxbian K.D., Lei B., Hoff J.S., Parkins L.D.
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.R., Parkins L.D.
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
emergence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49911 MW; 7CCE44F4026E3975 CRC64;
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GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0008243; F:plasminogen activator activity; IEA.

GO; GO:0008215; F:protein binding; IEA.

InterPro; IPR004093; Staphylokinase.

InterPro; IPR008124; Staphylokinase.

Pfam; PP02821; Staphylokinase; 3.

PRINTS; PR01753; STREPKINASE.
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EMBL; AE014169; AAM80305.1; -; Genomic DNA.

EMBL; BA000034; BAC64795.1; -; Genomic DNA.

HSSP; P00779; 114D.
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Mismatches:
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STRAIN-SF370 / ATCC 700294 / Serctype M1;

STRAIN-SF370 / ATCC 700294 / Serctype M1;

MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;

Perretti J.J., McShan W.M., Ajddc D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Ain Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., An Ann X., Clifton S.W., Roe B.A., McLandhin R.E.;

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. SG1. U.S.A. 98:4653 (2001).

"I - FUNCTION: This protein is not a protease, but it activates plasminogen by complexing with it. As a potential virulence factor, it is thought to prevent the formation of effective fibrin barriers around the site of infection, thereby contributing to the invasiveness of the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                      GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1112
AspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsn 346
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                    STRAIN=SP130/13 / Serotype M1;
MEDLINE=89160264; PubMed=2646590;
Walter F., Siegel M., Malke H.;
"Nucleotide sequence of the streptokinase gene from a Streptococcus
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EMBL, AE006620; AAX34665.1; -; Genomic_DNA.
PIR; S02724; S02724.
HSPP; Q53284; 1C4P.
SMR: P10520; 63-398.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR008124; Streptokinase.
PRINTS; PR01733; STREPKINASE.
COMPLETE Protecome; Plasminogen activation; Signal; Virulence.
SIGNAL.
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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Nucleic Acids Res. 17:1261-1261(1989).
                                                                                                                                                                                                                                                                                                            Name=ska; OrderedLocusNames=SPy1979;
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ID Q7X072, STRPY PRELIMINARY;
AC Q7X0Y2;
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DT 01-OCT-2004 (TERMBLEE). 25,
DT 01-MAR-2004 (TERMBLEE). 25,
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VOLEOTIDE SEQUENCE.

STRAIN=86-779;

PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;

Kalia A., Bessen D.E.;

Wildrutal selection and evolution of streptococcal virulence genes involved in tissue-specific adaptations.";

J. Bacteriol. 186:110-121(2004).
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Streptokinase.
Name-ska;
Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
[NGBL TaxID=1314;
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                 207 AspThrLysLeuLeuLysLeuAlaIleGlyAspThrValThrSerGlnGluLeuLeu
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STRAIN=IRPI12;
A Ralia A., Bessen D.E.;
Kalia A., Bessen D.E.;
Thubmed=14679231; DOI=10.1128/JB.186.1.110-121.2004;
Kalia A., Bessen D.E.;
Thatural selection and evolution of streptococcal virulence genes involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).
R. MEL; AY234130; AAP39950.1; -; Genomic_DNA.
R. SMR; OXX0Y7; 63-398.
GO; GO:0016301; P:kinase activity; IEA.
GO; GO:0016301; P:kinase activity; IEA.
GO; GO:0008243; P:plasminogen activator activity; IEA.
GO; GO:00515; P:protein binding; IEA.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR008124; Streptokinase.
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X PubMed=146/9231; DOI=10.1128/JB.186.1.110-121.2004;
Kalia A., Bassen D.B.;
I Natural selection and evolution of streptococcal virulence genes
involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).
II. Bacteriol. 186:110-121(2004).
IR BMB; AV34136; AAP39956.1; -; Genomic_DNA.
IRSP: Q5244; 1C4P.
SMR; Q7X0Y2; 63-398.
GO; GO:0006301; F:kinase activity; IEA.
RO; GO:0006313; F:plasminogen activator activity; IEA.
RO; GO:000515; F:protein binding; IEA.
RITEFPC; IPR004093; Streptokinase.
RITEFPC; IPR0041093; Streptokinase.
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                           Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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PRINTS; PR01753; STREPKINASE.
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                                                                   NCBI_TaxID=1314;
Streptokinase.
                                                       Streptococcus.
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PubMed=15272401; DOI=10.1086/422697;

PubMed=15272401; DOI=10.1086/422697;

Banks D.J., Porcella S.F., Barbian W.D., Beres S.B., Philips L.E.,

Banks D.J., Porcella S.F., Martin J.M., Somerville G.A., Musser J.M.;

Ray Voyich J.M., Deleo F.R., Martin J.M., Somerville G.A., Musser J.M.;

Ray Progress toward characterization of the group A Streptococcus

The regenome: complete genome sequence of a macrolide-resistant serotype

R. T. Infect. Dis. 190:727-738(2004).

R. ERRI, CP000003; AAT87827.1; -; Genomic_DNA.

R. S.RR, G.S.976; 63-398.

G.J. GO:0016787; F:hydrolase activity; IEA.

G.J. GO:0016301; F:hydrolase activity; IEA.

G.J. GO:0016319; F:plasminogen activator activity; IEA.

G.J. GO:0016319; F:plasminogen activator activity; IEA.

R. FREPPO: IPR004093; Staphylokinase.

R. Fram; PF02811; Staphylokinase.

R. Pram; PF02811; Staphylokinase.

R. R. Fram; PR01753; STREPKINASE.
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                                          GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
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                                                                                    TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAATCTC
                                                                                                                                                                                               33 ATAGCTGGTCCTGAATGGCTACTAGATCGTCCTCTGTAAATAACAGCCAATTGGTTGTT
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
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Matches:
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SEQUENCE 440 AA; 50160 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      Streptokinase (EC 3.4.-.-).
OrderedLocusNames=M6_Spy1692;
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1758.00
93.21%
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64.73%
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Q5X9T6 STRP6 PRELIMINARY;
Q5X9T6;
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HisLeuAla 409
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NCBI_TaxID=301450;
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Best Local Similarity:
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                                          1C5AF07907EC7AC8 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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Pfam; PF02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
                                         50160 MW;
                                                                                3.3e-117
1758.00
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                                                                                                                                                                                                                                                                                                                   M18
                                                                                                                                                                                                                                STRAIN=MGASS232 / Serotype M18;

MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;

A Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S. Sylva G.L., Sturdeant D.B., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Rapur V., Daly J.A., Veasy L.G., Musser J.M., Porcella S.F., Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever group A Streptococcus strains associated with acute rheumatic fever group A Streptococcus strains associated with acute rheumatic fever group A Streptococcus strains associated with acute rheumatic fever group A Streptococcus strains associated with acute rheumatic fever a cutobacks, AED 10107; AAL98517.1; -; Genomic_DNA.

EMBL; AE010107; AAL98517.1; -; Genomic_DNA.

RSP; OSNZA6; 63-398.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0016301; F:kinase activity; IEA.

R GO; GO:0016301; S:protein binding; IEA.

InterPro; IPR004033; Staphylokinase.

R InterPro; IPR004033; Staphylokinase.
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                                                                                                                                    OrderedicousNames=spyM18 2042;
Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Streptokinase.
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Matches:
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Mismatches:
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                                                        440 AA
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                                                      PRT;
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                                        GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGGCAAGGCTTAAGTCCAAAATCA
                                                                                                                                                  AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC
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187 ArgTyrThrValGlnPheThrProLeuAsnProAspAspAspAspPheLysProValLeuLys
         Kalia A., Bessen D.E.;

"Natural selection and evolution of streptococcal virulence genes
"natural selection and evolution of streptococcal virulence genes
involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).

EMBL; AY234134; AAP39954.1; -; Genomic_DNA.

HSSP; O53284; Ic4P.

GO; GO:0005315; P:kinase activity; IEA.

GO; GO:0005515; P:protein binding; IEA.

R GO; GO:0005515; P:protein binding; IEA.

InterPro; IPR004093; Staphylokinase.

R ThrerPro; IPR004124; Streptokinase.

R PRINTS; PR01753; STREPKINASE.
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PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;
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Q1-OCT-2003 (TEMBLrel. 25, Last sequence update)
Q1-OCT-2003 (TEMBLrel. 26, Last annotation update)
MAR.2004 (TEMBLrel. 26, Last annotation update)
Name=8ka;
Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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56	Qy         753 TTTACTTACCGGGTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 812           Db         267 PheThrTyrHisVally98AsnArgGluGlnAlaTyrGlnAsnAspAsnLysThrGlyLeu 286	AAAAAGGG 87	873 GADAAGCCGTATGATCGCAGTCACTTGAACTGTCACCATCAATACGTT 93	933 GATGTCGATACCAATGCTAAAAAGTGAGCGGCTCTTAACAGCTAGCGAAGGTAGCGAACGTAGC 99 327 ABPValabpThrLysaspLeuleulysSerdluGluGluculeulhrhrkassergluArgasn 34	ACAATCTC 10	Qy         1053 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGGAGATAATCACGATGAC         1112           Db         367 AspAlaPheAspIleMetAspTvTThrieuthrGlvivsValGluaspAshHiaAshTva 386	1113 ACCAACCGTATCATAACCGTTTTGGCAAGCGACCGAAGGAGAAATGCTACCTAC	1173 CATTAGCT 1181	Db 407 HisteuAla 409	RESULT 15 QYXQYO STREY D OZXOYO STREP DRELIMINARY. DRT. 440 AA	07X0Y0; 01-OCT-2003 (TEMBLEE]. 25, 01-OCT-2003 (TEMBLEE]. 25,	01-MAR-2004 (TrEMBLrel. Streptokinase. Name=ska:	Streptococcus pyogenes. Streptococcus pyogenes. Barteria. Firmicutes. Lartcharillales. Strentococcase	מודבלים מוחים מוחים מוחים		PubMed=14679231; DOI=10.1128/JB.186. Kalia A., Bessen D.E.;		RL J. Bacteriol. 186:110-121(2004). DR EMBL; AY234138; AAP399958.1; -; Genomic_DNA. DR HKKD: OK1284: 174D			InterPro; IPROC InterPro; IPROC		KW Kinase. SQ SEQUENCE 440 AA; 50143 MW; 4ACB2C29349D680C CRC64;	Scores:	5.95e-114 Lengin: 440 Score: 1715.00 Matches: 325 Percent Similarity: 91.91% Conservative: 27	

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Unclassified.  REFERENCE 1 (bases 1 to 1242) AUTHORS Reed,G.L. TITLE Bacterial fibrin-dependent plasminogen activator JOURNAL Patent: US 6210667-A 5 03-APR-2001; FRATURES 11242 Source /organism="unknown" /mol_type="unassigned DNA"	Query Match Best Local Similarity 99.7%; Pred. No. 1.9e-291; Matches 1151; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Qy         183 ATTGCTGGACCTGGGCTGCTAGACCGTCCATCTGTCACACACA	Qy         243 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACTTAGTCTTAAATTTTTTGAAATC         302	QY         303 GATCTAACATCAGGACTGATGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA 362	QY         363 AAACCATTIGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA         422           Db         181 AAACCATTIGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA         240	QY         423 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTCAGGTC 482	Qy 483 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC 542	Qy 543 AAAGATGGTAGCGTAACCTTGCCGACCAACTGTCCAAGAATTTTTGCTAAGCGGACAT 602	Qy 603 GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGGGAAATCTGTTGATGTG 662 	Qy 663 GAATAIACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 722	Qy 723 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 782	Oy 783 GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 842	Qy 843 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACCATTTTACCAATGGATCAAGAG 902	Qy 903 TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 962	Qy         963 AATGAAGAAATAAACAACACAGACCTGACCTGAGAAATATTACGTCCTTAAAAAAGGG 1022	Qy 1023 GAAAAGCGTATGATCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 1082
	Qy 600 CATGTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGGGAAATCTGTTGAT 659 Db 1561 CATGTGCGCGTTAGACCATATAAAGAAACCAATACAAAACCAAGGAAATCTGTTGAT 1620	QY 660 GTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTC 719	QY 720 AAAGATACTAAAGCTATTGAAACACTAGCTATCGGGGACACCATCACATCTCAAGAATTA 779	OY 780 CTAGCTCAAGGACAAAGGATTTTAAACAAAAACCACGCCCAGGCTATACGATTTATGAACGT 839 Db 1741 CTAGCTCAAGGACAAAAGGATTTTAAACAAAAACCACCAGGCTATACGATTTATGAACGT 1800	OY 840 GACTCCTCAATGGTCATGACAATGACAATTTTCCGTAGGATTTTACCAATGGATCAA 899	OY 900 GAGITIACITIACOGGITTAAAAATCGGGAACAAGGTIATAGGATCAATAAAAAATCIGGT 959	OY 960 CTGAATGAAGAAATAAACAACGGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAA 1019	OY 1020 GGGGAAAAGCCGTATGATCGTTTGATCGCAGTCACTTGAACTGTTCACCATCAATAC 1079	Qy 1080 GTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGT 1139	Qy 1140 AACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAAAT 1199 Db 2101 AACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAGTCTACTACAAAAT 2160	OY 1200 CTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGAT 1259	OY         1260 GACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGC 1319           Db         2221 GACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGC 2280	Oy 1320 TATCATTTAGCCGGTGGT 1337	O 1940 -	ARITATOO 1742 DP DNA 11MEAI ON Sequence 5 from patent US 6210667. N AR144000.1 GI:15105867	SOURCE Unknown. ORGANISM Unknown.

TTGCTGACAAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAA GCGGACATGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAACCAAGCGAAATCTG	715 GTCTCAAAGATACTAAGCTATTGAAAACACTACTGCGTGACACCATCACGTTCTCAAG 774  11	AACGTGACTCCTCAATCGTCATGACAATGACATTTTCCGTACGATTTTACCAATGG	895 ATCAAGAGTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGATCAATAAAAAT 954		902 ANCOIMACTINGACTILAGAGAITINIACGAICCICGIGAIAAGGICAAGATACICICACA 1021 1195 ACAATCTCGAIGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATC 1254 1022 ACAATCTCGAIGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATC 1081	1255 ACGATGACACCGTATCATAACCGTTTATATGGGCAAGCGACCGAAGGAGAATG 1314 1082 ACGATGACACCGTATCATAACCGTTTATATGGCAAGCGACCGAAGGAGAATG 1314 1082 ACGATGACACCAACCGTATCATAACCGTTTATATGGCAAGCGACCGAAGGAGAATG 1141 1315 CTAGCTATCATTTAGCCGGTGGT 1337 1142 TCAGCTATCATTTAGCCTATGAT 1164	T 4 C C ITION SION ON RDS	ORGANISM Streptococcus dysgalactiae subsp. equisimilis  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  Streptococcus.  Streptococcus.  AUTHORS Malke, H., Roe, B. and Ferretti, J.J.  TITLE Nucleotide sequence of the streptokinase gene from Streptococcus  equisimilis H46A  JOURNAL Gene 34 (2-3), 357-362 (1985)  PUBMED 298913  COMMENT.  COMMENT.
8 8 8 8 8	6 6 6	8 6 8	8 8 8 8	8 8 8 8	8 6 8	8 8 8	RESULT STRSKC LOCUS DEFINI ACCESS VERSIO KEYWOR SOURCE	REFEREN AUTHO TITLE TOURN COMMENT
		CATTRACCGGTGGT 1337		ORGANISM Unknown. Unclassified. Unclassified. Unclassified.  AUTHORS Hagenson, M.J. and Stroman, D.W. AUTHUE Yeast production of streptokinase JOURNAL Patent: EP 0148227-A1 5 09-DEC-1987; FRATURES Location/Qualifiers Source 11401 /organism="unknown"	ORIGIN  Query Match (69.2%; Score 1148.6; DB 6; Length 1401; Best Local Similarity 99.2%; Pred. No. 1.9e-291; Matches 1154; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	TTGCTGGACCTGGTGGCTGCTGCTCGTCCATCTGTCAACAACAACACGTTGTCAACACACAC	295 TTGAAATCGATCTAACATCACGACCTGCTCATGGAAAGACAGAGCAAGGCTTAAGTC 354	115   ACTTACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCACAGTAACGACTACT   174   174   175   176   176   177

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    .2568
/organism="Streptococcus dysgalactiae subsp. equisimilis"

GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
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Streptococcus dygalactiae subsp. equisimilis
Streptococcus dygalactiae subsp. equisimilis
Bacteria, Pirmicutes, Lactobacillales, Streptococcaceae,
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Ferretti,J.J. and Malke,H.
Ferretti,J.J. and Malke,H.
Ferrettekinase-coding recombinant vectors
Patent: EP 0151317-A 1 14-AUG-1985;
THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
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              J.J.Ferretti, 03-SEP-1957.

The -35 and -10 regions are located at positions 760-765 and 781-786 respectively and an SD sequence at 808-813. Downstream from the coding region inverted repeats (positions 2176-2190 and 2203-2217) are thought to function as transcription terminators. The nucleotide sequence of skc does not support the hypothesis that the gene has evolved by duplication and fusion, as suggested by internal two-fold AA homologies of its product.
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DLLKALQRQQLIANVHSNDDYERVIDESBARTITDRNGKYVFPADKDGSYTLPYQDYQB
PLLSGEHVRYRPYKEKPFLQVQAKSVDVBYTVQTPLNPDDDFRPGLKOTYLLKTLAIGD
TITSQELLAQAQSILNKNHPGYTIYERDSSIVTHDNDIFRTILPMDQEFTYRVKNREQ
AKTINKKGEGLARBINNTDLISRKYVLKKGEKPYDPPRISALLALTITKYDVDTINELL
KSEQLLITASERNLDPEDLYDENDKAKLLYNNLDAFGINDYTLIGKVEDNHDDTNRIIT
VYMGKRPEGENASYHLAYDKDRYTTEBERRVYSYLRYTGTPIPDNPNDK"
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/db xref="GI:153809"
/translation="MKNYLSFGMFALLFALTFGTVNSVQAIAGPEWLLDRPSVNNSQL
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Pred. No. 1.9e-291;
0; Mismatches 4;
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/note="prestreptokinase"
/codon_start=1
/trans1_table=11
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/product="streptokinase"
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/product="skc mRNA"
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Best Local Similarity 99.7%;
Matches 1151; Conservative
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1917 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1976
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/sub_species="equisimilis"
                                                                                                                                                              S.equisimilis dexb, abc, lrp, skc, X72832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hairpin loop"
complement (136. .1749)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="dexB"
complement(89..115)
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2989113
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/transl_table=11
                                                                           CATTTAGCCGGTGGT 1337
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              Indels
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 Pred. No. 1.9e-291;
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99.78;
            Conservative
Local Similarity
         Matches 1151;
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of the submitced seq:pSHD14/16, pSPV19, pSH2, pMF1,
pCWP73, pSH10, pWX4"
complement(89. .1761)
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|mol_type="genomic DNA"
|strain="H46A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-MAY-1993) H. Malke, Institute for Molecular Biology, Jena University, Winzerlaer Str 10, 07708 Jena, FRG Related sequences: K02986, M19346, X13399 & X13400.
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abc gene; ABC transporter; dexB gene; dextran glucosidase; glucan l,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel gene; akc gene; atreptokinase; stringent response-like protein. Streptococcus dysgalactiae subsp. equisimilis Streptococcus dysgalactiae subsp. equisimilis Bacteria; Firmicutes; Lactobacilales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 3621 to 6190)
Malke,H., Roe,B. and Ferretti,J.J.
Nucleotide sequence of the streptokinase gene from Streptococcus
equisimilis H46A
Loases 1 to 4188; 5790 to 8931)
Mechold, U., Steiner, K., Vettermann, S. and Malke, H.
Genetic organization of the streptokinase region of the
Streptococcus equisimilis H46A chromosome
Mol. Gen. Genet. 241 (1-2), 129-140 (1993)
                                                                                                                                                                                                                                                                                                                                                                    DNA linear BC rel genes and ORF1.
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TITSGELLAQAQSILAKNHFGYTI YERDSSI VTHDNDI FRTILEMDGBFTYRVKUREG
TYTSGELLAQAQSILAKNHFGYTI YERDSSI VTHDNDI FRTILEMDGBFTYRVKUREG
TYRI NKKSGLNBEINNTDLI SEKYTVLKKGEKPDPPDRSHLKLFTI KYVDVDTNELL
KSEQLLITASERNLDFRDKAKLLYNNLDAFGIMDYTLIGKVEDNHDDTRRI IT
VYMGKRPEGENASYHLAYDKDRYTEBEREVYSYLRYTGTPI PDNPNDK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="streptokinase"
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/note="unnamed protein product; ORF1"
                                                                                                                                                                                       4172. .4368
/note="static DNA bending locus"
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4395. .4400
/gene="skc"
4401. .4406
/gene="skc"
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                                                                                                                                                    note="TG motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /replace="gc"
6162. .6164
/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5796. .5837
/gene="skc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4439. .4516
/gene="skc"
5796. .5837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="ORF1"
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                                                                                                                                                                                                                                                4392. .5837
/gene="skc"
                                                                                                                           gene="lrp"
                                                                                                                                                                                                                                                                                                         4392. .4393
/gene="8kc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5007. .6009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="skc"
1439. .5761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="rel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="skc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                1392.
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Best Local Similarity
Matches 1151; Conserv
                                                                                           misc feature
                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                  -10_signal
                                                                                                                                                                                                                                                                                                                                                                                                  -10_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
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                         KQPDLAWENAHVRQKI YDMANPWIAKGIGGFRMDVIDLIGKIPDSBITCNGPRLHDYL
KEMNQAIFGNHDVMTVGETWGATPBIARQYSRPENKELSMVPQPEHVGLOHKPNAPKW
DYABELDVPALKTIPSKWQTELKLGEGWNSLFWNNHDLPRVLSIWGNDSIYREKSAKA
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LIALRKOQDMLVBAYHLLPTADKVFAXQRQFGEETYYIVVNVSDQEQVFAKOLAGAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GOA:Q54086"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MELKDYPPEMQVGPHPLGDKEWVSVKEGDQYVHPPKSCLSEKER
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QMIAGLEVILPISTTQTAFLCRQATSIKVLRSLEGLLPTLESDFGLALTMFVGNAWYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAAGTLRECFEBECOLLTAVLKOKSGGKLLTFAEVMIMSILGHOSFPALTROFHOFLN
POSDMADVVHALMSEHGNLVQTAQRLYIHRNSLQYKLDKFAQQSGLHLKQLDDLAFAY
LFLLKY"
HTSDEHAWFVEARENPNSPERDYYIWRDEPNNLMSIFSGSAWELDEASGQYYLHLFSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="(+1) frame shift mutation in H46A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="InterPro:IPR002197"
/db_xref="InterPro:IPR008931"
/db_xref="UniProt/Swiss-Prot:Q54087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl table=11
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/protein_id="CAA51350.1"
/db_xref="GI:407878"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="lrp"
/note="leucine zipper motif"
complement(4117. .4120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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/db_xref="GI:600072"
                                                                                                                                                                                                                                          complement (1757. .1761)
/gene="dexB"
complement (1780. .3051)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="abc"
/note="TG motif"
complement(3244. .4149)
                                                                                                                                                                                                                                                                                                                                         /gene="abc"
complement(1780. .1810)
                                                                                                                                                                                                                                                                                                                                                                                                  /gene="abc"
/note="hairpin loop"
complement (2482. .2499)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="abc"
/note="Walker motif A"
complement(2973. .2976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Walker motif B"
complement (2633. .2965)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (2828. .2854)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (3043. .3048)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (3050. .3051)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="lrp"
'note="hairpin loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="abc"
/note="alternative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (2644)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'депе="аbc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'депе="аbc
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RECOMBINATION VECTOR FOR PRODUCING STREPTOKINASE
PATENTON VECTOR FOR PRODUCING STREPTOKINASE
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PATENTOLEON CO

Streptococcus equisimilis
PD 26-NOV-1985
PD 26-NOV-1984
PD 1984212403
PP 09-OCT-1984 UP 1984212403
PR 10-OCT-1983 DB 3 255523, 02-MAR-1984 US 84 585417 PI
AIYOSEVU JIBI FURRETSUTEI, HORUSUTO MARUKE
PC CIENIS/00,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20,CIENI/20
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                                                                                                                                                                                                                                                      2568 bp DNA linear PAT 29-SEP-1997
PMF1 into which DNA encoding streptokinase

    .2568
/organism="Streptococcus dysgalactiae subsp. equisimilis"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           897 ATTGCTGGACCTGGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTAGTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .818
819. .896
/product='streptokinase signal peptide'
897. .2138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CC *Bo
                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC atti-sense: No;
CC *source: strain=Streptococcus equismilis H46A; CC |
Ilbrary=streptococcus equ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 2568;
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/db_xref="taxon:119602"
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C (C12N9/70,C12R1:19);
C strandedness Single;
C topology: Linear;
C hypothetical: No;
                                                                                                                                                                                                                                                                               DNA fragment of plasmid is inserted.
                                                                CATTTAGCCGGTGGT 1337
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selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D. and ramos gonz Lez,O.
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Vector for the production of transplastomic angiosperm plants
Patent: WO 2004/102926-A 26 08-APR-2004;
CENTRO DE INCENTERIA GENETICA Y BIOTECNOLOGIA (CU)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Nucleotide sequence of DNA fragment from the vector pVTPA-Estrep between the rice atpB and tobacco rbcL borders."
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               AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA
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PAT 20-APR-2004

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CQ797820 7057 bp DN Sequence 26 from Patent WO2004029256.

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A20015 SRQ ID NO: 23, Nucleotide sequence for methionol-streptokinase fusion protein.
A20015.1 GI:1247848
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RROSSIVTHDNID FRIILPHOQBFTYHVKNREQAYEINKKSGLNBEINKTDLISEKYYV
LKKGEKPYPDPDSKHLKLPTIKYVDVNTNELLKSEQLLTASERNLDPRDLYDPRDKAK
LLYNNLDAFGIMDYTTGKVEDNHDDTNRIITVYMGKRPEGENASYHLAYDKDRYTEE
RREVYSYLRYTGTPIPDNPNDK"
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                                                                                                                                                                                                                                                                      /organism="Streptococcus dysgalactiae subsp. equisimilis"
Mol Lype="genomic DNA"
/db xref="taxon:119602"
/noce="group: C"
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                                                                                1 (bases 1 to 1245)
Estrada,M.P., Hernandez,L., Perez,A., Rodriguez,P., Serrano,R.,
Rubiera,R., Pedraza,A., Padron,G., Antuch,W., de la Fuente,J. et
                                                                                                                                                                                                                                                                                                                                                                                          /note="streptokinase; Mature protein lacks initial Met"/codon start=1
/product="SKC-2"
                                                                                                                                                                                                    GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 115306] from the original journal article.
Location/Qualifiers
1. -1245
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              Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                          'gene="SKC-2"
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/gene="SKC-2"
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                                 ORGANISM
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       GGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATAC
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Dawson, K., Hunter, M.G. and Czaplewski, L.G.
Fibrinolytic and anti-thrombotic cleavable
Patent: US 5434073-A 25 18-JUL-1995;
Location/Qualifiers
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/organism="unknown"
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/product="methionyl-streptokinase fusion protein"
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KLLYNNLDAFGIMDYTLTGKYEDNHDDTNRIITVYMGKRPEGENASYHLAYDKDRYTE
ERREVYSYLRYTGTPIPDNPNDK"
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                                                                                                                                                                                                                                                                                                         GTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAA
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                                                                                                                                                                                           6; Length 1257;
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                                                                                                                                                                                        67.9%; Score 1127.6; DB 6;
larity 98.4%; Pred. No. 6.5e-286;
Conservative 0; Mismatches 19;
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Matches 1139; Conserv
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PHILLIPS PETROLEGUA CO

PHILLIPS PETROLEGUA CO

PN JP 1997296801-A/1

PD 24-DEC-1997 JP 1987109620

PR 08-MAY-1986 US 86 860960

PR MARIT JIEIN HEIJIENSON, DEEBUITSUDO UCOMATSUKU SUTOROCOMAN PC

C12N1S/00.C12N1/16,C12N9/12,(C12N1/16,C12R1:84); CC strandedness:

CC topology: Linear;

CC hypothetical: No;

FH Key Location/Qualifiers

FH FF T CDS | 8 . 1255

FT T CDS | Product='streptokinase'

FT 3'UTR | 1.756 . 1407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ATTCCATGATTGCTGGACCTGAGTGCTGCTAGACCGTCCATCTGTCAACAACAACTAT
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                                                                                                                                                                                                                                                                                                                                                                            67.8%; Score 1126.2; DB 6; Length
98.0%; Pred. No. 1.5e-285;
ive 0; Mismatches 23; Indels
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/product='streptokinase'
R 1. .7
Location/Qualifiers
                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/db xref="taxon:4081"
 24-DEC-1987;
Patent: JP 1987296881-A 1
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Best Local Simi
Matches 1140;
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DNA sequence of streptokinase.

N B01413.

E01413.

G1:2169669

JP 1987296881-A/1.

Lycopersicon esculentum (Solanum lycopersicum)

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; sterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

E 1 (bases 1 to 1407)

Marii, J. H. and Deebnitsudo, U.S.

YEAST DNA FRAGMENT AND ITS UTILIZATION
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              GACAAAGATGGTTCGGTAACCTTGCCGACCTGTCCAAGAATTTTTGCTAAGCGGA
                                GACAAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGA
                                                                       CATGTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGAT
                                                                                           GTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTC
                                                                                                                                                GIGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTC
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/bpotein_id="CAAOL487.1"
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KADLLKAIQEQLIANVHSNDDYFEVIDPASDATITDRNGKVYPADKDGSYTLPQPVQ
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DTITSQELLAQAQSILMKTHPCYTIYERDSSIYTHDNDIFRTILPMODBFTYHYKNR
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TVYMGKRPGGENASYHLAYDKDRYTEEREKEVYSYLRYTGTPIPDNPUNK
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                                                           AAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCA
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/organism="Bynthetic construct"
/mol_type="unassigned DNA"
/mol_type="taxon:32630"
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Patent: WO 9109125-A 24 27-JUN-1991;
Location/Qualifiers
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SEQ ID NO: 24; Nucleotide sequence
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A20016 A20016 GI:1247850
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ACAATCTCGATGCTTTTGGTATTATGGACTATACCTTTAACTGGAAAAGTAGAGGATAATC 1254
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                                                  1255 ACGATGACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAATG
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Dawson, K., Hunter, M.G. and Czaplewski, L.G.
Fibrinolytic and anti-thrombotic cleavable dimers
Patent: US 5434073-A 27 18-JUL-1995;
Location/Qualifiers
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January 31, 2006, 10:44:08; Search time 1004.11 Seconds (without alignments) 11024.772 Million cell updates/sec Run on:

US-09-940-235-10 1661 Title: Perfect score:

1 gcaacccgccagcctagcc......gaataagctgtaccatctaa 1661 Sequence:

Scoring table:

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4996997 seqs, 3332346308 residues Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaa37637 Chimeric		Aaa37628 Streptoki	Aaa37644 Chimeric	Aaa37643 Chimeric	Aaa37642 Chimeric	Aax80497 Streptoki	Aaq11651 FB-FB-SK		Aaa37633 S. equisi			Aax16632 Streptoco	Aax16633 Streptoco	Adm01294 Plasmid p	Aat77778 Coding se	Aan70106 DNA encod	Aag12158 Streptoki	Aaq20665 SKC-2 str
	QI .	AAA37637	AAA37622	AAA37628	AAA37644	AAA37643	AAA37642	AAX80497	AAQ11651	AAX80492	AAA37633	ABA05546	ABA05547	AAX16632	AAX16633	ADM01294	AAT77778	AAN70106	AAQ12158	AAQ20665
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æ	Query Match	100.0	77.2	73.4	71.3	70.2	69.2	69.2	69.2	69.2	69.2	69.2	69.2	69.1	68.9	68.4	68.3	67.8	67.8	67.7
	Score	1991	1282.2	1219.4	1185	1165.8	1150.2	1150	1148.8	1148.6	1148.6	1148.6	1148.6	1147	1143.8	1136.2	1134.6	1126.2	1126.2	1124.6
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Aaq12156 Streptoki	Aag12162 Factor Xa	Aaq12490 Factor Xa	OmpAL			Aat29961 Vector pS	Aaf82144 Mutant st	Aaz99251 DNA encod	DNA	Aaz99249 DNA encod	Aaz99250 DNA encod	Aaq12161 Met-core	Aaq12159 Truncated	Abn 70192 Streptoco	Adr83811 S. pyogen	Aaq05604 Streptoki		Aax83589 Recombina	Adf48644 Streptoco	Aag10230 Synthetic	Aax80494 Recombina	Aaa35009 Human ade	Acd06169 Human cDN	Adr90518 Human cDN	Adn95947 Human NOV
AAQ12156	AAQ12162	AAQ12490	AAQ12160	AAQ05603	AAN50493	AAT29961	AAF82144	AAZ99251	AAZ99252	AAZ99249	AAZ99250	AAQ12161	AAQ12159	ABN70192	ADR83811	AAQ05604	AAX80493	AAX83589	ADF48644	AAQ10230	AAX80494	AAA35009	ACD06169	ADR90518	ADN95947
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67.7	67.7	67.7	67.7	67.2	66.7	9.99	66.2	0.99	66.0	65.6	65.6	65.0	64.9	59.9	59.9	59.6	58.8	58.5	54.1	45.9	27.1	19.1	19.1	19.1	19.1
1124.6	1124.6	1124.6	1124.6	1116.6	1108.6	1107	1099.4	1096.6	1096.6	1089.2	1089.2	1080.4	1078.8	995	995	990.2	976.2	971.6	899.4	762.8	450	316.8	316.8	316.8	316.8
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## ALIGNMENTS

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Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy;
                                                                                                                     Streptococcus dysgalactiae subsp. equisimilis.
Homo sapiens.
Chimeric.
                                                                                                                                                                                                                   (COUL ) CSIR COUNCIL SCI IND RES.
                                                                      Chimeric SK-FBD coding sequence.
               AAA37637 standard; DNA; 1661 BP
                                                                                                                                                                                                    98IN-DE003825.
                                                                                                                                                                                    99EP-00310541.
                                                                                              plasminogen; human; fibronec cardiovascular disorder; ss.
                                                       (first entry)
                                                (revised)
                                                                                                                                                    EP1024192-A2
                                                                                                                                                                                   23-DEC-1999;
                                                                                                                                                                                                    24-DEC-1998;
                                              15-SEP-2003
13-OCT-2000
                                                                                                                                                                    02-AUG-2000.
                               AAA37637;
RESULT 1
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Sahni G, Kumar R, Roy C, Rajogopal K, Nihalani D, Sundaram V; Yadav M;

WPI; 2000-516032/47.

Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.

Example 5; Fig 19b; 58pp; English.

This sequence represents a chimeric streptkinase-fibrin binding domain (SK-FBD) protein coding sequence. The invention relates to a hybrid

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plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, and fibrin binding regions of human fibronectin, which are from fibrin binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ablidty to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating conversion of the plasmin of the adjust of the protein and the local plasmin of the adjust of the protein and the local plasmin of the plasmin of the adjust of the vascular system without significantly activating the circulating conversion of the plasmin of the protein and the local plasmin of the plasmin of the protein and the plasmin of the plasmin
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plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field) Sequence 1661 BP; 529 A; 370 C; 357 G; 405 T; 0 U; 0 Other;	<pre>uery Match 100.0%; Score 1661; DB 3; Length 1661; est Local Similarity 100.0%; Pred. No. 0; atches 1661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	1 GCAACCCGGCAGCCTAGCCGGGTCCTCAACGACAGCACGATCATGCGCACCCGTGG 60 	61 CCAGGACCCAACGCTGCCCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGG 120 	121 AGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGAGAGATATACCA 180 	181 TGATTGCTGGACCTGAGTGGCTGCTGCCCATCTGTCAACAGCCAATTGGTTG 240 	241 TTAGCGTTCCTGGTACTGTTGAGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAA 300 	301 TCGATCTAACATCACGACCTGCTCATGGAGGAAGACAGAGCAAGGCTTAAGTCCAAAAT 360 	361 CAAAACCATTIGCTACTGATAGTGGCGGATGTCACATAAACTTGAGAAAGCTGACTTAC 420 	421 TAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACTTGGGG 480 	481 TCAITGATTTTGCAAGGATGCAACCAITACTGATCGAAGGCCAAGGTCTACTTTGCTG 540	541 ACAAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGAATTTTTGCTAAGGGGAC 600 	601 AIGTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGATG 660 	661 TGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCA 720

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& g	1141	ACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAAT 1200 
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q	1201	TCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATG 1260
ò	1261	ACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAGA
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q	1501	TTAACTIGCGAAAGTAAACCTIGAAGCTIGAAGACTTIGCTTTIGACAAGTACACTIGGGAACA 1560
ò	1561	CTTACCGAGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGGACTGTACCT 1620
q	1561	ctraccaagragaractrargagcarccraaagacrccargarcragaacrgraccr 1620
à	1621	GCATCGGGGCTGGGCGAGGAGAATAAGCTGTACCATCTAA 1661
qq	1621	GCATCGGGGCTGGGCGAGGGGGGGGGGGGGGGGGGGGGG
RESULT 2 AAA37622 ID AAA3 XX AC AAA3	762	standard; DNA; 1377 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a streptokinase-NTRN (SK-NTRN) gene (where NTRN stands for N-terminally repaired with native sequence). The invention claimes to a pybrid plasminogen activator (PA) comprises a polypeptide funion between streptokinase (SK), which are capable of plasminogen (PG) activation, and fibrin binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinneties of plasminogen activation that are distinct from that cof natural streptokinase in the natural rate of the catalytic conversion of plasminogen to plasmin (1.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating convercemes systemic plasminogen activation encountered during clinical use constructions. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
                                                                                       SK; hybrid plasminogen activator; fibrin binding region;
uman; fibronectin; thrombolytic therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACCCGTGGCCAGGACCCAACGCTGCCCGAGATCTCGATCCCGCGAAATTAATACGACT
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                                                                                                                                                                                                                                                                                                                                                                              Sundaram V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1282.2; DB 3; Length 1377; Pred. No. 0; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1377 BP; 465 A; 302 C; 265 G; 345 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                              Rajogopal K, Nihalani D,
                                                                                                                                                           Streptococcus dysgalactiae subsp. equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 11; 58pp; English.
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                                                                                                                        cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                            Kumar R, Roy C,
                     (first entry)
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                                                   Streptokinase-NTRN gene.
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                                                                                                        plasminogen; human;
                                                                                                                                                                                            EP1024192-A2
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15-SEP-2003
13-OCT-2000
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Yadav M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
                                                                                                                                                                                                                                                                          Streptokinase; SK; hybrid plasminogen activator; fibrin binding region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.4%; Score 1219.4; DB 3; Length 1327; 99.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overcomes systemic plasminogen activation encountered during of streptokinase. (Updated on 15-SEP-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1327 BP; 456 A; 279 C; 250 G; 342 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                               plasminogen; human; fibronectin; thrombolytic therapy;
cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nihalani D,
                                                                                                                                                                                                                                                                                                                                                    Streptococcus dysgalactiae subsp. equisimilis
1261 AATGCTAGCTATCATTTAGCCTATGAT 1287
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                                                                                                         AAA37628 standard; DNA; 1327
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                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                      Streptokinase-NTR gene.
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Yadav M;
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Pred. No. 0; 0; Mismatches

Best Local Similarity 99.1 Matches 1226; Conservative

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101 TAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAAC

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                                                                               CAACAACAGCCAATTGGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACAT
                                                                                                   121 AAATAACAGCCAATTGGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACAT
                                                                                                                                                          TAGTCTTAAATTTTTTGAAATCGATCTAACATCACGGCCTGCTCATGGAGGAAAGACAGA
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Length 1541;

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          Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
                                                                                                                                                                          Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy;
AGTAGAGGATAATCACGATGACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACC
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            GTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTTGGTATTATGGACTATACCT
                         GEGATAAGGCTAAACTTCTACAACAACAACTCGATGCTTTTGGTATTATGGACTATACCT
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                                                                                                                                                                                                This sequence represents a chimeric streptkinase-fibrin binding domain (SK-FBD) protein coding sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between strepcokinase (SK), which are capable of plasminogen (FG) activation, and fibrin binding regions of human fibronectin, which are from fibrin binding domains (FBD) 4 and 5 or 1 and 2. The hyprid PA possesses the ability to bind with fibrin independently and also characteristically retains a FG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human FG. The hybrid streptokinsse-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy;
GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                          TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
                                                                                       Tradactricadadatriratacgarccrcgrgaraaggcraaacracracaacaarcrc
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cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clote soon after introduction into the vascular system without significantly activating the circulating blood plasminogen to plasmin, thus aiding in the localisation of the plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
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bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proteolytic cleavage. This reduces the rate of elegradation of the streptokinase at least two-fold. The present sequence encodes a streptokinase and maltose binding protein fusion protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAG
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                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                    69.2%; Score 1150; 99.6%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptokinase and maltose binding protein fusion protein encoding cDNA.
                                            GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                      GATGTCGATACCAACGAATTGCTAAAAAGTGAGCCACCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                                        TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTACAACAATCTC
                                                                                                                                                                                               TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAACAATCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; error thrombosis; pulmonary embolism; erebral thrombosis; graft thrombosis; arterial thrombosis; ss.
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ACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAAC 1137
                   sequence. The FB fragment has selective affinity for fibrin, low affinity for fibrinogen, and minimal immunogenicity, imparting thrombus-targetting capability. See also AAQ11649 and AAQ11650
                                                                                                                                                                                                                                                                                 TIGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTG 472
                                                                                                                                                                                                              CGAAGATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACACCCCAATTAG
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   DNA encodes an FB-FB dimer linked to the streptokinase
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                               2221 GACACCGACGGTATCATAACGGTTTATATGGGGCAAGCGACCCGAAGGAGAGAATGCTAGC
                                                                                                                        GTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTGGACGT
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/label= streptokinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising cadministering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a boterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, careful in patients with a thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified
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                                                                                                                                 GTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTACTACAACA
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                                                                                 GTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTACAACA
                                                                                                                                                                                                                                                                                                                                                               Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes an isolated bacterial protein that
                                                                                                                                                                                                                                                                                                                                                                           nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis; se
                                                                                                                                                                                                                                                                                                                                         Streptococcus equisimilis native streptokinase encoding cDNA.
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substrate site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence encodes native streptokinase at least two-fold. The present sequence standardise OS field)
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Pred. No. 0;
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                         GATGTCGATACCAACGAATTGCTAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
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                                                                               GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                            TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACCAATCTC
                                                                                                                                                                                                                                   Sundaram V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         equisimilis streptokinase coding sequence.
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animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovacular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin fi.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen to plasmin, thus aiding in the localisation of the plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
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69.2%; Score 1148.6; DB 3; Length 1245;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1151; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1245 BP; 426 A; 267 C; 237 G; 315 T; 0 U; 0 Other;
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                                                                                                                   GATGCTTTTGGTATTATGGACTATACTTGGAAAAGTAGAGGATAATCACGATGAC
GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                                                            GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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            associated side effects. The present sequence is the streptokinase CDNA used in the construction of a Maxadilan-Streptokinase fusion protein. Maxadilan is a vasodilator peptide produced by the salivary gland of the New World sand fly
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and the use of lower doses of the thrombolytic
                                                                                                                                          T; 0 U; 0 Other;
                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                         DB 6;
                                                                                                                                                                                      Score 1148.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                          Seguence 1254 BP; 426 A; 271 C; 241 G; 316
                                                                                                                                                                                      69.28;
                                                                                                                                                                                                                                       Matches 1151; Conservative
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6055 GATCTAACATCACGACCTGCTCATGGAGGAAGAAGACAGGCGAAGGCTTAAGTCCAAAATCA
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                                                                                                                                                          5935 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGACACACAGCCAATTAGTTGTT
                                                                                                                                                                                             243 AGCGTTGCTGGTACTGTTGAGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6235 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
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                                                                                                                         183 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT
                                                                                                                                                                                                                                                                 303 GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA
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                Sequence 8893 BP; 2366 A; 2106 C; 2246 G; 2175 T; 0 U; 0 Other;
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                                                 Score 1148.6; DB 6
Pred. No. 3.3e-314;
0; Mismatches 4;
                                                 Query Match
Best Local Similarity 99.7%;
Matches 1151; Conservative
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            GATGTCGATACCAACGAATTGCTAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 966
                                                                     TTAGACTTCAGAGATTTATATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
                                                                                                                                             GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGGATAATCACGATGAC
                                                                                                                                                                                                                       TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAATCTC
                                                                                                                                                                                        New fusion protein or conjugate, useful for treating unstable angina, acute myocardial infarction or stroke, comprises a vasodilator polypeptide and a thrombolytic polypeptide, or active fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptokiname; cerebroprotective; cardiant; gene therapy; fumion; vamodilator; thrombolytic; angina; myocardial infarction; mtroke; gene therapy; maxadilan; mand fly; plasmid; dm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maxadilan-streptokinase fusion protein plasmid pTYB3maxstk
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                                                                                                              183 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACACAGCCAATTGGTTGTT
                                                                                                                                  1 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCACCAACAGCCGATTAGTTGTT
                                                                                                                                                                                        243 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC
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                                      Length 1242;
 Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;
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                                    Score 1147; DB 2;
Pred. No. 3.3e-314;
0; Mismatches 5;
                                    69.1%;
ilarity 99.6%;
Conservative
                                                        Similarity
                                                                         Matches 1150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus equisimilis H46A, streptokinase; mutant, fibrinolytic; plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin; serine protease; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction; fibrinolysis; resistance; ds.
                                    streptokinase polypeptide - useful as plasmin-resistant
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/note= "no stop codon given"
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                                                                                ATTGCTGGACCTGGTGGCTGCTGGCGTCCATCTGTCACCAACAGCCAATTAGTTGTT
                                                                                                                                                                                    GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a DNA vector (A) for stable transformation and expression of genes (I) in plastids, where (I) is inserted in an artificial intergene region (AIR) formed by combining two 5'-untranslated regions (5'-UTRS) of genes that transcribe in different directions and are derived from plants of different divisions or classes. (A) are used to produce transplastomic angiosperms that have improved agronomic properties (e.g. resistance to biotic or abiotic stress) or express a very wide range of agricultural, veterinary, pharmaceutical, nutritional or industrial products, e.g. enzymes, vaccinating antigens, cytokines or immunoglobulins. Use of (A) eliminates the need for a transposon for gene insertion; inserted genes do not require promoters and terminators; and the structure of flanking sequences in (A) can be eliminated by homologous recombination. (A) provides efficient and stable expression of genes without causing any functional alterations. This sequence
DNA vector for transformation and expression in plastids, useful e.g. for producing pharmaceutical proteins or improving agronomic properties, has gene inserted in artificial intergene region.
                                                                     vector; plastid; artificial intergene region; plant;
transplastomic angiosperm; agronomic property; stress resistance;
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Search completed: January 31, 2006, 18:17:50 Job time : 1005.11 secs

Sequence 16, Appl Patent No. 5455158 Sequence 1, Appli Sequence 135, Appl Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli

Sequence 15, Appl Sequence 13, Appl Sequence 11, Appl

Sequence 1, Sequence

Patent No. 5240845 Patent No. 5240845 Sequence 13, Appl Sequence 189, Appl Sequence (Appli Sequence (Appli Sequence (Appli

Sequence 3, Appl:

OM nucleic

Run on:

Sequence:

Minimum DB Maximum DB

Searched:

Database :

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Sequence 1, Application US/09211542A

Sequence 1, Application US/09211542A

Patent No. 6210667

Patent No. 6210667

TRIES OF INVENTION:

APPLICANT: Reed, Guy L.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWBERG & SUNSTEIN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FLING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Strimpel, Harriet M.
RESTERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-09-213-38
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US-08-259-569-16
US-08-25-888-16
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US-08-551-356-1
PCT-US93-12687-1
US-09-513-12687-1
US-09-913-118-3
US-09-913-718-3
US-09-813-718-3
US-09-813-718-1
 US-09-211-542A-3
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US-09-813-718-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BROMBERG & SUNSTEIN, LLP STREET: 125 Summer Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2385 base pairs TYPE: nucleic acid STRANDEDNESS: single
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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LOCATION:
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January 31, 2006, 16:24:19; Search time 293.256 Seconds (without alignments) 10068.109 Million cell updates/sec
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Sequence 5, 1
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Sequence 19,
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

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7: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-07-854-596B-14
US-07-854-596B-42
US-07-854-596B-46
US-07-854-596B-46
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Maximum Match 100%
Listing first 45 summaries
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1080.4
1078.8
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DB 3; Length 2385;

Result

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                                                                                                                                                                                                                                                                 Sequence 5, Application US/09211542A

Patent No. 6210667

GENERAL INFORMATION:

APPLICANT: Reed, Guy L.

ITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWHERG & SUNSTEIN, LLP
STREET: 125 Summer Street
                                          1260 GACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAAGAAATGCTAGC
                                                                 2221 GACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAAAAAACGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCGCCAATTGGTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1148.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Stimpel, Harriet M.
REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
FILECOMMUNICATION INFORMATION:

MELECOMMUNICATION INFORMATION:

MELECOMMUNICATION INFORMATION:

MELECOMMUNICATION INFORMATION:

MELECOMMUNICATION INFORMATION:

MELECOMMUNICATION INFORMATION:
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Best Local Similarity 99.7%;
Matches 1151; Conservative
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TELEFAX: (617)443-0004
INFORMATION FOR SEQ ID NO: 5: SEQUIENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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COUNTRY: USA
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IOCATION:
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Sequence 1, Application US/08568393B Patent No. 5876999

RESULT 3 US-08-568-393B-1

ANTI-SERSE: N ORIGINAL SOURCE: ORGANISM: Streptococcus equisimilis H46A ORGANISM: Streptococcus equisimilis H46A INDIVIDUAL ISOLATE: Malke, H., Roe, B., and Ferretti, J. J.; INDIVIDUAL ISOLATE: "Nucleotide sequence of the streptokinase gene from Strepto INDIVIDUAL ISOLATE: equisimilis H46A" from Gene 34:357-362 (1985). CELL TYPE: Streptococcus equisimilis H46A ö 242 302 180 240 300 362 422 482 542 9 243 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC 241 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGCAAGGCTTAAGTCCAAAATCA AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC Gaps ; Length 1242; l streptokinase thrombolytic agents 5; Indels Suite 69.1%; Score 1147; DB 2; 99.6%; Pred. No. 0; iive 0; Mismatches 5; APPLICANT: Hua-Lin Wu
APPLICANT: Guey-Yueh Shi
TITLE OF INVENTION: Preparation of novel streg
TITLE OF SEQUENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeing & Chang
STREET: TWO NO. 5876999th Second Street, Sui
CITY: San Jose
STATE: California
COUNTRY: USA COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB
MEDIUM TYPE: Storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPEFECT 6.1 on Window 3.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,393B
FLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chi-Ping Chang
REFRENCE/DOCKET NUMBER: 37,798
REFRENCE/DOCKET NUMBER: 37,798
REFRENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (408) 288-8385 INFORMATION FOR SEC ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1242 base pairs TYPE: Nucleic Acid STRANDENBSS: double TOPOLOGY: linear MOLECULE TYPE: Best Local Similarity 99.6 Matches 1150; Conservative Similarity HYPOTHETICAL: N ANTI-SENSE: N US-08-568-393B-1 61 121 363 181 483 303 423 Query Match 셤 ò

셤 ò 원 δ 면 ò 원 δ 셤 ઠ g ò q ઠે 셤 ਨੇ 원 ò g ò 셤 ò a ò 셤 ઠ 셤 ò

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LOCATION: DNA sequence No. 5876999174 and 175 have been changed LOCATION: from AA to GG, and PROTEIN sequence No. 587699959 has been changed LOCATION: from Lys to Glu.
OTHER INFORMATION:
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99.4%; Pred. No. 0;
ive 0; Mismatches 7; Indels 0;
              TELEPAX: (408)289-8386
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1242 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: double
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Matches 1148; Conservative
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301 ATTGATTTTGCAAGCGATGCAACCATTACTGAAACGGCAAGGTCTACTTTGCTGAC 360
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                                                                   361 AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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Patent No. 5876999
GENERAL INFORMATION:
APPLICANT: Hua-Lin Wu
APPLICANT: Guey-Yueh Shi
TITLE OF INVENTION: Preparation of novel streptokinase
TITLE OF INVENTION: mutants as improved thrombolytic agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Jeing & Chang
STREET: Two No. 5876999th Second Street, Suite 290
CITY: San Jose
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US-08-568-393B-2
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                                                                                                                                                                                                                                                                                                                             Score 1134.6;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                          05433/009001
                   NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,919
REFRENCE/DOCKET NUMBER: 0543
TELEPHONE: 617/542-8076
TELERAX: 617/542-8906
TELERAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2566 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                     A MOLECULE TYPE: DNA (genomic) US-08-488-940-19
                                                                                                                                                                                                                                                                                                                             68.3%;
99.5%;
   ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 99.5
Matches 1149; Conservative
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APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STRATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READBRE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-UNN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08488940 Patent No. 5854049
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                                                       gene
human plasminogen
                                                     Properties: Streptokinase gene
The gene product binds to human plasminoge
The gene product is an activator of human
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0
                                                                                                                                                      Length 1245
                                                                                                                                                                                         0; Mismatches 17; Indels
                                                                                                                                                      DB 2;
                                                                                                                                                    67.9%; Score 1127.8; 98.5%; Pred. No. 0;
             FEATURE: from 1 to 1245 bp mature peptide OTHER INFORMATION: Properties: Streptoki OTHER INFORMATION: The gene product bind OTHER INFORMATION: The gene product bind OTHER INFORMATION: The gene product is not streptoki
ATCC-9542 strain
                                                                                                                                                                                         Matches 1138; Conservative
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IMMEDIATE SOURCE:
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Patent No. 5296366
GENERAL INFORMATION:
APPLICANT: Garcia,M.P.E. et al
TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTOKINASE, NUCLEOTIDE SEQUENCE
TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTOKINASE, NUCLEOTIDE SEQUENCE
TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTOKINASE, NUCLEOTIDE SEQUENCE
TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTOKINASE, NUCLEOTIDE SEQUENCE
TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTOKINASE, NUCLEOTIDE SEQUENCE
TITLE OF INVENTION: OF A GENE WHICH COMPANY INCHARGES FOR STREET: PARKWAY 109 Office Center, 328 Newman Springs Road,
STREET: P. O. Box 8489
COUNTRY: USA
COUNTRY: USA
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                                                                                                                                                                       GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1262
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                                                                                                                                                                                                                                                                                                                                                                                   1975 ACCAACGIATCATAACGITTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGCTAT 2034
                                                                                                                                                                                                                                                    1855 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
                     AATGAAGAAATAAACCACACACAGACCTGAGTCTCTGAGAAATATTACGTCCTTAAAAAAAGGG
                                                                                              GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                                                    1083 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGGCTAGCGAACGTAAC
AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAGGG
                                                                                                                                                                                                                               1143 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
                                                                       GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY.

ZIP: 07701
COMPUTER READBLE FORM:
MEDIUM TYPE: 3 1/2" 1.44Mb IBM compatible diskette
COMPUTER: 1BM PS/2 Model 80
COMPUTER: 1BM PS/2 Model 80
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Microsoft Word for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/703,778D
FILING DATE: 19910522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1245 base pairs
TYPE: NUCLEOTIDE WITH CORRESPONDING PROTEIN
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19910522
CLASSIFICATION: 435
ATORNEY AGENT INPORMATION:
NAME: MIChaelson, Peter L.
REGISTRATION NUMBER: 30090
REFERNCE/DOCKET NUMBER: Centro-1
TELEPHONE: (908)530-654
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1245 base pairs
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US-07-703-778D-1
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                                                                                                      GAIGCITITIGGIAITATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1262
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                                                                                                                                                                                                                                                                       /note= "Methionyl-streptokinase
fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
TILLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Dr. John J. McDonnell
Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: MCDORNELL, John J
REGISTRATION NUMBER: 26,949
REPERENCE/DOCKEY NUMBER: 92,33
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-715-1000
TELEFAX: 312-715-1234
TELEFAX: 312-715-1200
TELEFAX: 312-715-1200
TELEFAX: 312-715-1200
SEQUENCE CHARACTERISTICS:
LENGTH 1257
LENGTH 
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LOCATION: 1..1257
OTHER INFORMATION: /not
OTHER INFORMATION: fusi
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; LOCATION: 4..1248
US-07-854-596B-25
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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LOCATION: 4..1248
FEATURE:
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1140 AACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAAT 1023
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    Length 1257
                                              Indels
  DB 2;
                                                 19;
67.9%; Score 1127.6;
98.4%; Pred. No. 0;
ive 0; Mismatches
Query Match
Best Local Similarity 98.4
Matches 1139; Conservative
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                                                                                                                      554 TTGAGGTCATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACT
                                                                                                                                                                                                                                                                                                                                                                                                    614 TIGCTGACAAAGAIGGTICGGTAACCTIGCCGACCCCAACCTGTCCAAGAATTTTIGCTAA
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                                                                  314 TAGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTT
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STREET: Ten South mac...

CITY: Chicago
STATE: 11

COUNTRY: USA
ZIP: 60666
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UN-1992
CLASSIFICATION: 43
ATTORNEY/AGENT INFORMATION:
NAME: MCDOMPOLI, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 26,949
TELECHONE: 312-715-1000
TELECHONE: 1312-715-11334
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fused to a yeast alpha-factor"
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APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Caplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                 3: Dr. John J. McDonnell
Ten South Wacker Drive, Suite 3000
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98.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                         Sequence 27, Application US/07854596B
Patent No. -5434073
                                                                                                                                      TATCATTTAGCCGGTGGT 1337
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1..1512
OTHER INFORMATION: /note:
OTHER INFORMATION: fused
FRATURE:
NAME/KEY: CDS
LOCATION: 7..1503
FEATURE:
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Best Local Similarity 98.0
Matches 1140; Conservative
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LOCATION: 7..1503
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MOLECULE TYPE: CDNA
FEATURE:
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US-07-854-596B-27
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187 GACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAAGGCTTAAGTCCAAAAATCA
                                                                                  247 AAACCATTTGCTACTGATAGTGGCGCGATGCCACATAAACCTTGAAAAAGCTGACTTACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACTTAGTCTTAAATTTTTTGAAATC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGGCAAGGCTTAAGTCCAAAATCA 362
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                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEM: NC-DOS/MS-DOS
SOFTWARE: PATEM: NC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATOONEY/AGENT INFORMATION:
NAME: MCDONNIAL] John J
REGISTRATION NUMBER: 26,949
REFERRNCE/DOCKET NUMBER: 26,949
REFERRNCE/DOCKET NUMBER: 32,337
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mature
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                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Dawson, Keith M
APPLICANT: Czaplewski, iloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1317
OTHER INFORMATION: // note= "Ompal fused to
OTHER INFORMATION: streptokinase gene"
FAATURE:
NAME/KEY: CDS
LOCATION: 4..1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.7%; Score 1124.6; Best Local Similarity 98.4%; Pred. No. 0; Matches 1136; Conservative 0; Mismatches
                                 CTAGCTATCATTTAGCCTATGAT 1416
                                                                                                                                                      Sequence 18, Application US/07854596B
                CTAGCTATCATTTAGCCGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: mat_peptide
LOCATION: 4..1308
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                RESULT 9
US-07-854-596B-18
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US-07-854-596B-18
              1315
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Best Local
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985 GATGTCAACACCAACGAATTGCTAAAAAGCGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1044
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                                                                                                                                                385 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
                                                                                                                                                                                                                                                               445 AAAGATGGTTCGGTAACCTTGCCGACCCACTGTCCAAGAATTTTTGCTAAGCGGACAT
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                                                                                                                   483 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
                                                                                                                                                                                                                               543 AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
                                                                                                                                                                                                                                                                                                                                             GTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
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Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1323 CATTTAGCCGGTGGT 1337
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US-07-854-596B-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTTATTTTTGAAATT 204
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                                                                                                                                                                                                                                                            ADDES.__
STREET: Ten ._
CITY: Chicago
STATE: IL.
COUNTRY: USA
COMPUTER: ILM PC COMPATIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-UNN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDOMMINI, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
THE TELECOMMUNICATION INFORMATION INFORMATION
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                                                                                                        APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1124.6;
Pred. No. 0;
0; Mismatches
                       Sequence 14, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Stre
equisimilis"
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TELEX: 910-221-5317
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.4%;
Matches 1136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: 1..1335
OTHER INFORMATION: dquis:
FEATURE: NAME/KEY: CDS
LOCATION: 7..1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: mat_peptide
LOCATION: 7..1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
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US-07-854-596B-14
US-07-854-596B-14
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                                               568 AAAGATGGTTCGGTAACCTTGCCGACCCCAACTGTCCAAGAATTTTTGCTAAGCGGACAT
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US-07-854-596B-46
Sequence 46, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Hunter, Michael G
APPLICANT: Capplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
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fusion linked by Factor Xa cleavable IEGR"
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TITLE OF INVENTION: Proteins and nucleic acids NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS: 7
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDOINGIL, John J
REGISTRATION NUMBER: 26,949
REFERRATION NUMBER: 26,949
REFERRATION NUMBER: 26,949
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1000
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 98.4%;
Matches 1136; Conservative (
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NAME/KEY: misc_feature
NCATION: 1..1458
OTHER INFORMATION: /note
OTHER INFORMATION: fusion
PEATURE:
NAME/KEY: CDS
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FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1449
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STRANDEDNESS: single
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US-07-854-596B-42
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
APPLICANT: Czaplewski, Lloyd G
NUMBER OF SEQUENCES: 73
CORRESPONDENCES: 73
CORRESPONDENCE ADDRESS:
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATTTAGCCGGTGGT 1337
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STATE: IL
COUNTRY: USA
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fusion linked by Factor Xa-cleavable IEGR"
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Pred. No. 0;
0; Mismatches 19; Indels 0;
                                                MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIPICATION: 435
ATCONEY/AGENT INFORMATION:
NAME: McDonnell John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10F021-5317
TELECOMMUNICATION 10F021-5317
TELECOMMUNICATION 10F0 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
MAINTENET TOWN: Innear
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Best Local Similarity 98.4%;
Matches 1136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: mat_peptide
; LOCATION: 1..1449
US-07-854-596B-46
                  ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..1467
OTHER INFORMATION: OTHER INFORMATION: FEATURE: NAME/KEY: CDS
LOCATION: 1..1449
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                                                                                                                                                                                   TCCTCAATCGTCACTCATGACATGACATTTCCGTACGATTTTACCAATGGATCAAGAG
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                                                     GATACTAAAGCTATTGAAAAACACTAGCTATCGGTGACACCATCACAACTCTCAAGAATTACTA
                                                                                                         GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
                                                                                                                                                                                                                                                                                                                                                                             AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       907 GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                               GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
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APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Galvo, Ariana Garcia
APPLICANT: Becalona, Elder Pupo
APPLICANT: Becalona, Elder Pupo
APPLICANT: Griego, Martha De Jesus Gonzalez
ITILE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFRENCE: Sequence Listings 1-14 re: 976-5
Patent No. 6309873
CURRENT APPLICATION NUMBER: US/09/374,038
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Streptococcus equisimilis US-09-374-038-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09374038; Patent No. 6309873; GENERAL INFORMATION:
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US-09-374-038-13
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                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: 1..2589
OTHER INFORMATION: /note=
OTHER INFORMATION: /OmpAL-Streptokinase-streptokinase fusion linked
OTHER INFORMATION: by thrombin-cleavable VELQGVVPRG"
FRATURE:
NAME/KEY: CDS
LOCATION: 4..2580
FRATURE:
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Best Local Similarity 98.4%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches
; NAME/KEY: mat peptide
; LOCATION: 4..2580
US-07-854-5968-34
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Qy 1260 GACACCAACCGTATCATAACCGTTTATATGGGCAAGCGA 1298 	RESULT 15 US-09-658-179-13 ; Sequence 13, Application US/09658179 ; Patent No. 6413759 ; GENERAL INFORMATION: ; APPLICANT: Madrazo, Isis Del Carmen Torrens ; APPLICANT: Garcia, Jose De Jesus De La Fuente		щ	C	; LENGTH: 1122 ; TYPE: DNA ; TYPE: DNA ; ORGANISM: Streptococcus equisimilis	0	SCACCTGAGTGGCTGCTAGACCTCCATCTGTCAACACCCAATTGGTT 23	240 GTTAGCGTTGCTGGTACTGTTGAGGGACGAATCAAGACATTAGTTTTTTGAA 	300 ATCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGAAGGCTTAAGTCCAAAA 121 ATTGACCTTAACATCACCACCTGCTTCATGAGGAGAAGAAGAAGAGAAGGCTTAAGTTCAACAAAAAGAAGAAGAAGAAGGTTAAGTTCAAAAA	360 TCAAAACCATTTGCTACTGATGGCGCGATGTCACATAAACTTGACAAAAGCTGACTTA		480 GTCATTGATTTTGCAAGCGATGCATTACTGATCGAACGGCAAGGTCTACTTTGCT	540 GACAAAGATIGGTICGGTAACCTTGCCGACCCTGTCCAGGATTTTTGCTAAGCGGA	600 CATGIGGGGGGTTAGACCATATAAAGAAAAACCAATACAAAACCAAAGCGAAATCTGTTGAT 	Qy 660 GTGGAATATACTGTTACTCCCTTAAACCCTGATGACGATCTCAGACCAGGTCTC 719	Qy 720 AAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTA 779 
180 ATGATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTT 239	240 GTTAGCGTTGCTGGTACTGTTGAGGGGACGAATGAGGACATTAGTCTTAAATTTTTTGAA 299	360 TCAAAACCATTIGCTACTGATAGIGGCGCGAIGICACATAAACTIGAGAAAGCIGACTIA 419 	420 CTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACTACTTTGAG 479 	480 GTCATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCT 539 	540 GACAAAGAIGGIICGGIAACCIIGCGACCCAACCIGICCAAGAAITITIGCIAAGCGGA 599 	600 CATGTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGGAAATCTGTTGAT 659 	660 GTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTC 719 		780 CTAĞCTCAAGCACAAAGCATTTTAAACAAAAACCACGCCCAGGCTATACGATTATGAACGT 839 	GACTCCTCAATGGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGG 	900 GAGITIACTTACCGTGTTAAAATCGGGAACAAGTTATAGGATCAATAAAAATCTGGT 959 	960 CTGAATGAAGAAATAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAA 1019 	1020 GGGGAAAAGCCGTATGATCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAATAC 1079 	1080 GTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCACCTCTTAACAGCTAGCGAACGT 1139 	AACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAAT 	1200 CTCGATGCTTTTGGTATTATGGACTATACTTAACTGGAAAAGTAGAGGATAATGACGAT 1259 

Search completed: February 1, 2006, 12:43:42 Job time : 294.256 secs Н

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January 31, 2006, 17:06:30; Search time 1372.44 Seconds (without alignments) 10008.068 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 10, Appl Sequence 5, Appli Sequence 6, Appli Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 574, Appl Sequence 63, Appl Sequence 63, Appl Sequence 75, Appl Sequence 654, Appl Sequence 664, Appl Sequence 664, Appl Sequence 654, Appl Sequence
SUMMARIES	US-09-940-235-10 US-09-940-235-5 US-09-940-235-6 US-09-940-235-9 US-09-940-235-1 US-09-940-235-1 US-09-940-235-1 US-09-940-235-1 US-09-940-235-1 US-09-940-235-1 US-10-44-792-657 US-10-44-874-874 US-10-171-1311-63 US-09-940-874-874 US-10-171-14-87-97-97 US-10-182-9364-75 US-10-171-18-95 US-10-18-18-18-18-18-18-18-18-18-18-18-18-18-
DB	
Length	1661 1327 1327 1327 1328 1329 1329 1329 1329 1329 1329 1329 1329
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Result No.	22222222222222222222222222222222222222

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US-10-477-173-654	US-10-852-335A-52	US-10-447-161-4	US-10-450-763-22270	US-09-940-235-3	US-10-084-817-2	US-10-210-120-49	US-10-956-157-4288	US-10-909-035-49	US-10-450-763-22266	US-10-144-194A-51	US-10-491-566-51	US-10-236-392-3	US-10-956-157-4995	US-10-098-841-6	US-10-447-161-8	US-10-734-564-27	US-10-852-335A-53	US-10-287-436A-81	US-10-098-841-5	US-10-098-841-8	US-10-098-841-7
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19.1	19.1	19.1	19.1	19.0	18.9	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8
316.8	316.8	316.8	316.8	316.4	313.6	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312
24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 10, Application US/09940235

Publication No. US2003005921A1

GENERAL INFORMATION:

APPLICANT: Kumar, Rajesh

APPLICANT: Rajesh

APPLICANT: Sahni, Girish

APPLICANT: Rajagopal, Kammara

APPLICANT: Rajagopal, Kammara

APPLICANT: Nihalani, Deepak

TITLE OF INVENTION: PROTEIN

FILE OF INVENTION: PROTEIN

FILE REFERENCE: 07064-099002

CURRENT PLILNG DATE: 2002-04-09

PRIOR FILING DATE: 1998-12-23

PRIOR PLILNG DATE: 1998-12-24

NUMBER OF SEQ ID NOS: 28

SEQ ID NO 10

LENGTH: 1661

TENDER PROTEIN: NINGOWS VERSION 4.0

LENGTH: 1661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 1661; Conservative
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DD   1201 TCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGATAATCAGATG   1260	RESULT 2  Sequence 5, Application US/08940235  Sequence 5, Application US/08940235  Sequence 5, Application No. US02030059921A1  APPLICANT: Rajsappal, Kammara  APPLICANT: Rajsappal, Kammara  APPLICANT: Rajsappal, Kammara  APPLICANT: No. No. Charactic StrepTOKINASE  STILLE OF INVENTION: PROTECTION SOCIETION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION: PROTECTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  SEQUENCE TO ANY AND A PROCESS FOR THE PREPARATION OF SALD  TITLE OF INVENTION NO. CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SALD  SEQUENCE TO ANY AND A PROCESS FOR THE PREPARATION OF SALD  TO SECURE TO ANY AND A PROCESS FOR THE PREPARATION OF SALD  TO SECURITY AND A PROCESS FOR THE PREPARATION OF SALD  TO SALD AND A PROCESS FOR THE PREPARATION OF SALD  TO SALD A SALD
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   CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR PILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR PILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: F8stSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 1541
                                                                                                                                                                                                                                               Query Match 71.3%; Score 1185;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1194; Conservative 0; Mismatches
                                                                                                                                                                                                       OTHER INFORMATION: Hybrid cassette
                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 9, Application US/09940235

Publication No. US2003005921A1

GENERAL INFORMATION:
APPLICANT: Sahni, Girish
APPLICANT: Rajagopal, Kammara
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINGEN ACTIVATION
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SA;
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
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US-09-940-235-13

Publication No. US20030059921A1

GENERAL INFORMATION:

APPLICANT: Rajesh

APPLICANT: Rajesh

APPLICANT: Rajesh

APPLICANT: Nihalani, Deepak

APPLICANT: Wihalani, Deepak

APPLICANT: Suhdavit

TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE

TITLE OF INVENTION: RAJESTING ALTERED PLASMINOGEN ACTIVATION

TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

TITLE OF INVENTION: PROTEINS DATE: 2090-204-09

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION NUMBER: US/09/940,235

CURRENT APPLICATION NUMBER: 09/471,349

PRIOR FILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-12-24

NUMBER OF SEC ID NOS: 28

SEQ ID NO 12

LENGTH: 2096

TUNDE OF NOTE OF SEC ID NOS: 28

LENGTH: 2096

TUNDE OF NOTE OF SEC ID NOS: 28

LENGTH: 2096

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ORGANISM: Artificial Sequence
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GENERAL INVERTION:

GENERAL INVERTION:

APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Rajesh
APPLICANT: Rajesh
APPLICANT: Rajespal, Kammara
APPLICANT: Rajegopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vaeudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT PAPLICATION NUMBER: 09/471,349
PRIOR APPLICATION NUMBER: 1999-12-23
PRIOR APPLICATION NUMBER: 1N 3825/DEL/98
PRIOR PILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
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                                                                                GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCCATCACATCTCTAAGAATTACTA
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                                                                                  Sequence 11, Application US/09940235

Bequence 11, Application Wo/09940235

Bedication No. US20030059921A1

GENERAL INFORMATION:

APPLICANT: Samin, Girish

APPLICANT: Samin, Girish

APPLICANT: Samin, Girish

APPLICANT: Sundaram, Vasudha

APPLICANT: Nihalani, Deepak

APPLICANT: Nihalani, Deepak

APPLICANT: Sundaram, Vasudha

APPLICANT: Sundaram, Vasudha

APPLICANT: Sundaram, Vasudha

APPLICANT: Sundaram, Vasudha

TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID

TITLE OF INVENTION: NUMBER: US/09/940,235

CURRENT FILING DATE: 2002-04-09

PRIOR FILING DATE: 1999-12-23

PRIOR PLING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: IN 3825/DEL/98

SOFTWARE: FastSEQ for Windows Version 4.0

SEQUENO: INVENTION: 110
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CATTTAGCTGGTGGTCGAGCGCAACAGATTGTAC 1764
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Hybrid cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-940-235-11
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                                                                                                                                                                                                     GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                    901 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                        TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
                                                                                         961 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTACAACAACCAATCTC
                                                                                                                                                      1021 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
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Sequence 657, Application US/10474792

Publication No. US20040236072A1

GENERAL INFORMATION:

APPLICANT: Olmsted, Stephen

APPLICANT: Olmsted, Stephen

APPLICANT: Minter, Lourie

TITLE OF INVENTION: SURPACE PROTEINS OF STREPTOCOCCUS PYOGENES

TITLE OF INVENTION NUMBER: US/10/474,792

CURRENT APPLICATION NUMBER: US/10/474,792

CURRENT APPLICATION NUMBER: US/10/474,792

SOFTWARE: PATENTIN DATE: 2003-10-14

SOFTWARE: PATENTIN VERBION 3.0

SEQ ID NO 657
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Pred. No. 3.6e-274;
0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-10-474-792-657
                                                                                                                                                                                                                                            CATTIAGCCGGTGGT 1337
                                                                                                                                                                                                                                                                     1141 CATTTAGCCTATGAT 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.9%;
Best Local Similarity 91.3%;
Matches 1055; Conservative
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US-10-474-792-657
                  1083
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                                                                                                                                                                      Indels
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                                                                                                                                         Score 1148.6;
Pred. No. 0;
0; Mismatches
 for Windows Version 4.0
                                        TYPE: DNA
ORGANISM: Streptococcus equisimilis
FEATURE:
                                                                                                                                       Query Match
Best Local Similarity 99.7%;
Matches 1151; Conservative 0
                                                                                               (1) ... (1242)
SOFTWARE: FastSEQ
SEQ ID NO 1
LENGTH: 1245
                                                                               ; NAME/KEY: CDS
; LOCATION: (1)
US-09-940-235-1
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APPLICANT: Peyman, John A

APPLICANT: Peyman, John A

APPLICANT: Reiger Daniel K

APPLICANT: Reiger Daniel K

APPLICANT: Shimkerb, Mark E

APPLICANT: Shimkerb, Richard A

APPLICANTON NUMBER: 140/236,392

CURRENT FILING DATE: 2000-00-33-0

PRIOR APPLICATION NUMBER: US09/540,763

PRIOR APPLICATION NUMBER: US09/635,949

PRIOR APPLICATION NUMBER: US09/635,949

PRIOR PILING DATE: 2000-08-10

PRIOR PILING DATE: 2001-09-12

PRIOR PILING DATE: 2001-09-12

PRIOR PILING DATE: 2000-08-10

PRIOR PILING DATE: 2000-08-10

PRIOR PILING DATE: 2000-08-10

PRIOR PILING DATE: 2000-09-12

PRIOR PILING DATE: 2001-09-07

PRIOR PILING DATE: 2001-09-07
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                                                                                   MacDougall, John R
Malyankar, Uriel M
Miller, Charles B
Miller, Isabelle
Padigaru, Muralidhara
Perturajan, Meera
Pena, Carol A
     Kekuda, Ramesh
LaRochelle, William J
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ORGANISM: Homo sapiens
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LOCATION: (26)..(6986)
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US-10-236-392-1
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| Publication No. US20040067490A1
| GENERAL INFORMATION:
| APPLICANT: Boldog, Ferenc L
| APPLICANT: Burgess, Catherine, E
| APPLICANT: Casman, Stacie J
| APPLICANT: Casman, Stacie J
| APPLICANT: Catterton, Elina |
| APPLICANT: Catterton, Stacie J
| APPLICANT: Catterton, Stacie J
| APPLICANT: Cabtree, Julie |
| APPLICANT: Ellerman, Karen |
| APPLICANT: Gerlach, Valerie |
| APPLICANT: Gerlach, Valerie |
| APPLICANT: Grosse, William M |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTTAGCCGGTGGT 1337
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CTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTTACCGAGTGGGTGAACA

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132 GTAATGTGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAAC 191

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GENERAL INCARATION:

APPLICANT: Schiegel, Robert

APPLICANT: Chen, Yan

APPLICANT: Chao, Xumei

APPLICANT: Ananta, John

APPLICANT: Annatar, John

APPLICANT: Annatar, Mubhangi

APPLICANT: Ganravarapu, Manjula

APPLICANT: Ganravarapu, Manjula

APPLICANT: Hoersh, Sebsstian

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: OF CERVICAL CANCER

TITLE OF INVENTION: OF CERVICAL CANCER

TITLE OF INVENTION: OF CERVICAL CANCER

CURRENT APPLICATION NUMBER: US/10/171,311

CURRENT FILING DATE: 2001-06-13

PRIOR FILING DATE: 2001-11-14
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Pred. No. 4.2e-79;
0; Mismatches 2; Indels 0;
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
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Matches 318; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-824A-574
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US-10-171-311-63
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CURRENT APPLICATION NUMBER: US/10/831,704

CURRENT FILING DATE: 2002-05-23

PRIOR PILING DATE: 1996-102-23

PRIOR PILING DATE: 1996-12-23

PRIOR PILING DATE: 1996-12-23

PRIOR PILING DATE: 1996-12-24

PRIOR PILING DATE: 1999-12-24

PRIOR PILING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 191

SOPTHARE: FREEEEQ for Windows Version 4.0
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Sequence 574, Application US/09964824A
GENERAL No. US20020102531A1
GENERAL NO. US20020102531A1
APPLICANT: HORINGAN, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
             CTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGG 1638
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llarity 99.4%; Pred. No. 4.2e
Conservative 0; Mismatches
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Sequence 38, Application US/10831704
Publication No. US20550100931A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 318; Conserv
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LENGTH: 7679
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                                                                                          Length 7680;
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APPLICANT: Jensen, Roderick V.
APPLICANT: Gullans, Steven R.
APPLICANT: Gullans, Steven R.
APPLICANT: Gullans, Steven R.
APPLICANT: Gullans, Steven R.
TILLE OF INVENTION: Diagnostic and Prognostic Tests
FILE REPERENCE: B00801/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236,031B
CURRENT APPLICATION NUMBER: US 60/317,389
PRIOR PILING DATE: 2002-09-05
PRIOR PILING DATE: 2002-09-05
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.1
SEQ ID NO 69
                                                                                       19.1%; Score 316.8; DB 5; 99.4%; Pred. No. 4.2e-79;
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Pred. No. 4.2e-79;
0; Mismatches 2;
                                                                                                      Pred. No. 4.2e-79;
0; Mismatches 2;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 63
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Best Local Similarity 99.4%;
Matches 318; Conservative
                                                                                                   Best Local Similarity 99.4
Matches 318; Conservative
                                     TYPE: DNA
ORGANISM: Homo sapiens
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US-10-236-031B-69
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                                                     ; ORGANISM: Hon
US-10-171-311-63
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                   GTAATGTTGGTTTGTTATTGTTATTGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAAC
                                                                                   CTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACA
                                                                  CTGAAGCTGAAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACA
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; ORGANISM: Homo sapiens
US-10-374-979-75
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US-10-374-979-75
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Sequence 75, Application US/10182936A

Sequence 75, Application US/10182936A

Publication No. US20040038860A1

GENERAL INFORMATION:

APPLICANT: Anisowicz, Anthony

APPLICANT: Banagnez, Veronique

APPLICANT: Banagnez, Veronique

APPLICANT: Paworsky, Paul

TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions

FILE REFERENCE: 032796-143

CURRENT APPLICATION NUMBER: US/10/182,936A

CURRENT PILING DATE: 2002-08-02

PRIOR PILING DATE: 2002-09-17

PRIOR PILING DATE: 2002-09-17

PRIOR PILING DATE: 2003-09-05-17

PRIOR PILING DATE: 2003-03-04

PRIOR PILING DATE: 2002-03-04

PRIOR APPLICATION NUMBER: US 60/353,058

PRIOR PILING DATE: 2002-03-04

PRIOR PILING DATE: 2002-03-04

PRIOR PILING DATE: 2002-03-04

NUMBER OF SEQ ID NOS: 216

SEQ ID NO 75

LENGTH 7680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1579 CITATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAG 1638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 CTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGGGG 311
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Pred. No. 4.2e-79;
0; Mismatches 2; Indels
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Best Local Similarity 99.4%;
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-182-936A-75
US-10-182-936A-75
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Search completed: February 1, 2006, 14:21:19 Job time : 1373.44 secs

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January 31, 2006, 18:17:59 ; Search time 307.097 Seconds (without alignments) 4492.841 Million cell updates/sec
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/ cgn2_6/prodata/2/pubpna/USO6_NEW_PUB.seq:*
/ cgn2_6/prodata/2/pubpna/USO6_NEW_PUB.seq:*
/ cgn2_6/prodata/2/pubpna/USO9_NEW_PUB.seq:*
/ cgn2_6/prodata/2/pubpna/USO9_NEW_PUB.seq:*
/ cgn2_6/prodata/2/pubpna/USO9_NEW_PUB.seq:*
/ cgn2_6/prodata/2/pubpna/USI0_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6059551 seqs, 415333918 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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1661
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		-631	-631	10-631-558-6	10-631-558-	10-631-558-	10-631-558	10-631-558-	10-631-558-3	10-821-234-	10-995-561-	10-995-561-	10-995-561-1	10-995-561-	10-995	10-995	10-995-561	10-995-561	10-995	10-995-561-:	10-995-561-1	-995	10-995
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118-11-136-507-0446	10000	US-10-995-561-1323/	US-10-995-561-4446	US-10-995-561-4450	US-10-995-561-4468	US-10-995-561-4486	US-10-995-561-4503	US-10-995-561-4522	US-10-995-561-4541	US-10-995-561-4560	US-10-995-561-4575	US-10-995-561-4592	US-10-995-561-4596	US-10-995-561-4621	US-10-995-561-4640	US-10-995-561-27119	US-11-094-586-17	US-11-076-733-86	US-11-076-733-87	US-11-137-395-9	US-11-149-403-34	US-11-149-403-33	US-11-149-403-35
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## ALIGNMENTS

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Sequence 10, Application US/10631558

Sequence 10, Application US/10631558

Publication No. US20050260598A1

GENERAL INFORMATION:

APPLICANT: Kamar, Rajesh

APPLICANT: Rajespal, Kamara

APPLICANT: Rajespal, Kamara

APPLICANT: Rajespal, Kamara

APPLICANT: Sundaram, Vasudha

APPLICANTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

FILE REFERENCE: 07064-009002

CURRENT FILING DATE: 2003-07-31

PRIOR FILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 10

LEBROTH: 1661

TWOR THE MENTER DATE: 1000-1000

MARCHARIA DATE: 1000-100

MARCHARIA D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCAACCCGCCAGCCTAGCCGGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGG 60
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100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 1661; Conservative
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1201 TCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAGTAGAGGATAATCACGATG 1260   1201 TCGATGCTTTTGGTATTATGGACTATACTGGAAAAGTAGAGGATAATCACGATG 1260   1201 TCGATGCTTTTTGGTATTATGGACTATACTGGAAAAGTAGAGGAAAAGCTAGAT 1220   1261 ACACCAACCGTTACTATACTAGACGCAAGCGAGCCCCGAAGGAAG	RESULT 2  US-10-631-588-5  US-10-631-588-5  SEQUENCE 5, Application US/10631558  SEQUENCE 5, Application No. US20052056058A1  SEQUENCE 7. Sundaman No. US20052056058A1  APPLICANT: Sabni, Girish APPLICANT: Sabni, Girish APPLICANT: Rajagopal Asmara APPLICANT: Rajagopal Asmara APPLICANT: Rajagopal Asmara APPLICANT: Sundaman, Vandah, ITILB OP INVENTION: NOVEL CACT-SPECIFIC STREPTOKINASE ITILB OP INVENTION: PROTEIN PROFESSING ALITERED PLASMINOGEN ACTIVATION TITLE OP INVENTION: PROFESSING ALITERED PLASMINOGEN ACTIVATION TITLE OF INVENTION: PROFESSING ACTIVATION TITLE OF INVENTION ACTIVATION TITLE OF INVENTION ACTIVATION ACTIVATION TITLE OF INVENTION ACTIVATION ACTIVATION TITLE ACTIVATION ACTIVATION A
CCAGGACCCAACGCTGCCCGAGATCTCGCTTAATAATTAAT	601 ATGTGGGGGTTAGACCATATAAGAAAACCAATACAAAACCAAGGGAAATCTGTTGATG 601 ATGTGGGGGAATACCATATAAGAAAAAACCAATACAAACCAAGCGAAATCTGTTGATG 601 ATGTGGGGGAATACCATATAAAAAAAAAAAAAAAACCAAGAAACCAAGCTAAACCAAGATTTCAAGACCAAGCTCCAA 601 TGGAATATACTTGAAAACACTTCCCTTAAACCCTGATGACATTTCAGACCAGGTCTCA 721 AAGATATACTTAAAAACACTTGAAAACCCTGATCAACATTTCAGACCAGGTCTCA 721 AAGATACTAAGCTATTGAAAACACTGCTACCGTGAACACATCAACATCAACAATTAC 721 AAGATACTAAGCTATTGAAAACACTGCTACCGTGAACACATCAACATCCAAGAATTAC 721 AAGATACTAAGCAAAACACAAAAACAAAAAACACACACAC

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APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TYTLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION WINDER: US/10/631,558
CURRENT FILING DATE: 2003-07-31
PRIOR PLILING DATE: 1099-12-23
PRIOR PLILING DATE: 1999-12-23
PRIOR PLILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 9
LENGTH: 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTTGTTTAACTTTAAGAAGGAGATATACCATGATGATAGCTGGTCCTGAATGGCTACTAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                      71.3%; Score 1185; D 98.8%; Pred. No. 0; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Best Local Simi
Matches 1194;
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Sequence 9, Application US/10611558
Publication No. US20050260598A1
GENERAL INFORMATION:
APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Ray, Chait
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                                      ATTGATTTTGCAAGCGATGCCATTACTGATCGAAAACGGCAAGGCTTACTTGCTGAC
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Publication No. US20050260598A1
GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Rahi, Girish
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
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APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION NUMBER: US/09/940,235
PRIOR FILING DATE: 1999-12-23
PRIOR PELING DATE: 1999-12-24
SPRIOR PELING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10631558; Publication No. US20050260598A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
                                                                                                                                                                                                                                                     RESULT 6
US-10-631-558-11
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LENGTH: 1782
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us-10-51-584-5

; Sequence 3, Application US/10631558

; Publication No. US20050260598A1

; GENERAL INFORMATION:

; APPLICANT: Runar, Rajesh

; APPLICANT: Sahni, Girish

; APPLICANT: Ray, Chait

; APPLICANT: Ray, Chait

; APPLICANT: Ray, Chait

; APPLICANT: Ray whavit

; APPLICANT: Sundaram, Vasudha

; APPLICANT: Yadav, Mahavit

; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINGEN ACTIVATION

; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID

; TITLE OF INVENTION: PROTEIN

; FILM REFERENCE: 07064-009002

; CURRENT FILING DATE: 2003-04-09

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 09471,349

; PRIOR APPLICATION NUMBER: 09471,349

; PRIOR PILING DATE: 1999-12-24

; NUMBER OF SEQ ID NOS: 28

; SOFTPARARE: PRESEQ FOR Windows Version 4.0
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              TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
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ORGANISM: HOMO
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; LOCATION: (1)
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APPLICANT: Yadav, Mahavir

TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT PELLING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PRESENCE OF WINDOWS VERSION 4.0
SEQ ID NO 1
LENGTH: 1245
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                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(1242)
US-10-631-558-1
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Publication No. US20050272054A1
GENERAL INPORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: US/10/995,561
TITLE OF INVENTION: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PEASEEG for Windows Version 4.0
SEQ ID NO 105
LENGTH: 2488
                                                                                                                                                                                                                                            APPLICANT: CARGILL.
TITLE OF INVENTION: GENETIC POLYMORPHISNS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 114
LENGTH: 2443
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Pred. No. 4.2e-87;
1; Mismatches 5;
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                                                             1639 GGAGAATAAGCTGTACCATC
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Best Local Similarity 98.1%;
Matches 314; Conservative
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US-10-995-561-114
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US-10-995-561-105
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                                                                            121 AATGTGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCT
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
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     19.0%; Score 316.4; DB 7; Length 777; 99.7%; Pred. No. 6.5e-89;
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18.8%; Score 312; DB 7;
Best Local Similarity 98.4%; Pred. No. 6.7e-87;
Matches 315; Conservative 0; Mismatches 5;
                   Pred. No. 6.5e-89;
0; Mismatches 1
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 693, Application US/10821234; Publication No. US20050255114A1; GENERAL INFORMATION:
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SOFTWARE: DL SEQ genes Version 1.0
SEQ ID NO 693
LENGTH: 8232
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Query Match
Best Local Similarity 99.77
Matches 317; Conservative
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US-10-821-234-693/c
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     CTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGCGCGAG 1638
                                                                                                                                                                                                                                                                  APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEG ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 117
LENGTH: 7823
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOOLISS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NO 111
                         704 CTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATYGGGGCTGGGGCGAG 763
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                                                                                                                                                                                                                ; Sequence 117, Application US/10995561; Publication No. US20050272054A1; GENERAL INFORMATION:
                                                                               1639 GGAGAATAAGCTGTACCATC 1658
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CORGANISM: Homo sapiens
US-10-995-561-117
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US-10-995-561-117
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Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS AND DRUG RESPONSE, METHODS (FILE OF INVENTION: DRECTION AND USES THEREOF
TITLE OF INVENTION: DRECTION AND USES THEREOF
TITLE OF INVENTION: DATE: 1004-11-24
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PASTESEQ for Windows Version 4.0
SEQ ID NO 112
LENGTH: 6510
                                                                                                                                                                                                                            584 GCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAAC
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                                                                           Score 311.6; DB 7;
Pred. No. 4.3e-87;
1; Mismatches 5;
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Pred. No. 7.8e-87;
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98.1%;
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Best Local Similarity 98.1%;
Matches 314; Conservative
                                                                     Query Match
Best Local Similarity 98.1'
Matches 314; Conservative
             CRGANISM: Homo sapiens US-10-995-561-105
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ORGANISM: Homo sapiens
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US-10-995-561-112
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US-10-955-561-113
i Sequence 113, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
    TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
    TITLE OF INVENTION: DETECTION AND USES THEREOF
    TITLE OF INVENTION: DETECTION AND USES THEREOF
    TITLE OF INVENTION: DETECTION AND USES THEREOF
    CURRENT APPLICATION NUMBER: US/10/995,561
    CURRENT PILING DATE: 2004-11-24
    NUMBER OF SEQ ID NOS: 85702
    SOFTWARE: PSetSEQ for Windows Version 4.0
    LENGTH: 7935
                                                                                                                                 | GTAATGTGTTGTTTGTATGCAGGAAGCCGAGGTTTTAACTGCGAAAGTAAAC 1518
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                                                                        Score 311.6; DB 7; Length 7848;
Pred. No. 8.7e-87;
1; Mismatches 5; Indels 0;
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Best Local Similarity 98.1%; Pred. No. 8.8e-87;
Matches 314; Conservative 1; Mismatches 5;
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                                                                      Query Match
Best Local Similarity 98.1%;
Matches 314; Conservative 1
; LENGTH: 7848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-111
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ORGANISM: Homo sapiens
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January 31, 2006, 16:09:44; Search time 6825.35 Seconds (without alignments) 11385.988 Million cell updates/sec
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                                                                                                                                                               US-09-940-235-10
1661
1 gcaaccccgccagcctagcc......gaataagctgtaccatctaa 1661
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                     41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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9b est4: *
9b est6: *
9b est7: *
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Perfect score:
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	TITLE Shotgun sequencing o		_	G	COMMENT Contact: Simpson A.J	_	Ludwig Institute for	Rua Prof. Antonio Pr	Brazil	Tel: +55-11-2704922	Fax: +55-11-2707001	Email: asimpson@ludw	This sequence was de	Project. This entry	(http://www.ludwig.o	011100-466-g03&t3=20	Seq primer: puc 18 f	High quality sequenc	High quality sequenc	FEATURES Location/Qu	source 1480	"-msinem-"	/mol type="	/db xref="t	/dev stage=	/clone_lib=
	_				Ś															FE?						_
			Description	******************	BF993488 QV0-GN021	CN332340 170005325	CN332343 170005314	CN332334 170004554	CN332338 170006001	CN419479 170004706	AL603362 DKFZp686C	CN332332 170005326	DR004705 TC124975	CN332335 170005322	CN332342 170005339	AL706288 DXFZp686P	BX473413 DKFZp6861	BX398838 BX398838	DQ039102 Homo sapi	BX640608 Homo sapi	BX640875 Homo sapi	BX439175 BX439175	BX473425 DKFZp686L	BX473443 DKFZD686P	BX473395 DKFZp686D	BX473392 DKFZp686C
SOUMMENTES			ID		BF993488	CN332340	CN332343	CN332334	CN332338	CN419479	AL603362	CN332332	DR004705	CN332335	CN332342	AL706288	BX473413	BX398838	1 DQ039102	HSM806653	HSM806992	BX439175	BX473425	BX473443	BX473395	BX473392
			DB C		7	7 7	7 7	7	5 7	3 7		1 7	8	5 7	7	т _	'n	2	;; _	4	4		s S	. 5	s S	5
			Lengt		480	597	657	099	999	673	9/9	684	693	706	716	751	765	911	7434	7868	8411	1038	683	715	749	759
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		,	Score		312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	311.6	311	311	311	311

BF993485 OV0-GN021	_	_	AL706197 DKFZp6861	AL706221 DKFZp686J	BX473391 DKFZp686C	BX473407 DKFZp686G	BX380583 BX380583		BX417945 BX417945		CR749281 Homo sapi	BX510005 DKFZp6861	DR005445 TC109245	DQ039103 Pan trodl	BF751799 RC3-BN042	BF988908 IL5-GN017	CR749317 Homo sapi	CR791105 DKFZp469C	AW068245 cn23g07.y	BX380854 BX380854	BX473387 DKFZp686B	CN332337 170005326
BF993485	BQ366579	BX501294	AL706197	AL706221	BX473391	BX473407	BX380583	BX386270	BX417945	CR749316	CR749281	BX510005	DR005445	. DQ039103	BF751799	BF988908	CR749317	CR791105	AW068245	BX380854	BX473387	CN332337
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18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.6	18.6	18.6	18.5	18.3	18.3	18.2	18.1
310.4	310.4	310.4	310.4	310.4	310.4	310.4	310.4	310.4	310.4	310.4	310.4	310	310	310	308.8	308.8	308.8	307.8	304.4	303.6	303	301
23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

BF993488 QVO-CN0216-011100-466-g03 GN0216 Homo sapiens CDNA, mRNA sequence. BF993488.1 GI:12399811 EST. Homo sapiens (human) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;	Homindae, Homo.  Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., O'Hare, M.J., Gooliveira, P.S., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  Simpson, A.J.  Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  10737800  Contact: Simpson A.J.G.  Laboratory of Cancer Genetics  Ludwig Institute for Cancer Research  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  Rall: +55-11-2704922	Fax: +55-11-2707001  Fax: +55-11-2707001  This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-GN0216-01100-466-g03&t3=2000-11-01&t4=1)  Seq primer: puc 18 forward  High quality sequence start: 24  High quality sequence start: 24  High quality sequence start: 24  I ocation/Qualifiers  I ocation/Qualifiers    cation/Qualifiers   1 ocation/Qualifiers   1
RESULT 1 BP993488 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL PUBMED COMMENT	FEATURES SOUFCE

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EST 16-MAY-2004

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/note="Organ: placenta\_normal; Vector: puc18; Site\_1:

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/clone lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
HI (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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1 (bases 1 to 657)

1 (bases 1 to 657)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L. W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                               GTAATGTGTTTGGTTTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAAC
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17000531483454 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
CN332343
                                                                                                                                     Length 597;
                                                                                                                                   18.8%; Score 312; DB 7; Length 59 98.4%; Pred. No. 3.2e-78; ive 0; Mismatches 5; Indels
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Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenbergergeron.com
Insert Length: 657 Std Brror: 0.00.
Location/Qualifiers
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Geron Corporation
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I (bases 1 to 597)

S Handenberger, R., Waei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
Transcriptone characterization elucidates signaling networks that
Control human ES cell growth and differentiation

L Nat. Biotechnol. 22 (6), 707-716 (2004)

D 151461197

Contact: Brandenberger R
Regenerative Medicine
Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 7760
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               Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                           2; Length 480;
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                                                                                                                                                                       18.8%; Score 312; DB 2;
llarity 98.4%; Pred. No. 3e-78;
Conservative 0; Mismatches
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Insert Length: 597 Std Error: 0.00.
Location/Qualifiers
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/mol type="mRNA"
/db xref="taxon:9606"
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/tissue_type="embryonic stem cell, retinoic acid and micogen-treated hBS cell line H7"
/clone_lib="GNN PRENEU"
/note="oligo dT primed, full-length enriched cDNA library from hBS cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
                                                                                                                                                                                                            GTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAAC 1518
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17000600181351 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 666)

1 standenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
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230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                18.8%; Score 312; DB 7; Lv 98.4%; Pred. No. 3.3e-78; ive 0; Mismatches 5;
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Insert Length: 666 Std Error: 0.00.
Location/Qualifiers
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Regenerative Medicine
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CN332338.1 GI:47332272
                 conditions."
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Homo sapiens
                                                                                                                          Best Local Similarity 98.4
Matches 315; Conservative
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from embryoid body outgrowths derived from hBS cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
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1 (bases 1 to 660)

1 (bases 1 to 660)

1 (bases 2 to 660)

1 (bases 3 to 660)

1 (bases 3 to 660)

1 (bases 4 to 660)

1 (bases 5 to 60)

1 (bases 6 to 660)

2 (bases 6 to 660)

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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                             467 CTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACA
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17000455431365 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
CN332334
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                                                                                                                                                 Score 312; DB 7; Length 657; Pred. No. 3.3e-78; 0; Mismatches 5; Indels
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Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
121: 650 473 8658
Fax: 650 473 7760
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Insert Length: 660 Std Error: 0.00.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                              Query Match
Best Local Similarity 98.4%;
Matches 315; Conservative (
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Gaps

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372

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432

492

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AL603362

676 bp mRNA linear EST 04-SEP-2003
DKFZp686C197_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686C197_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKZ); but a "wiemann@dkfz" heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
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1 (bases 1 to 676)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       German Genome Project.

No sl sequence available.

This clone (DKFZp68G197) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                                                                                                                                                                                                                                     313 GCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAAC
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Pred. No. 3.3e-78;
                         Indels
                    5;
98.4%; Pred. No. 3.3e-78; ive 0; Mismatches 5
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/db_xref="taxon:9606"
/clone="DKFZp686C197"
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Matches 315; Conservative
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/clone lib="GRN EB"
/note="oligo dT pimed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
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Nat. Biotechnol. 22 (6), 707-716 (2004)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
                                                                                                                                       417 GCAATGCGTTGCTTGTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAAC
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                  Length 666;
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                                                             Indels
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Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 673 Std Error: 0.00.
Location/Qualifiers
                  Score 312; DB 7;
Pred. No. 3.3e-78;
0; Mismatches 5;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Regenerative Medicine
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                Query Match
Best Local Similarity 98.4%;
Matches 315; Conservative
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DEFINITION

RESULT 6 CN419479 LOCUS

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS source

ORIGIN

FEATURES

PUBMED COMMENT

JOURNAL

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Hominidae; Homo.

E I (bases I to 633)
S liv.X., Poster, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L., Liu, X., Porter, J., Sadhs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Zhang, X., Jay, G. and He, W.
High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
Unpublished (2005)
Contact: Kovacs, KF
High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com )
6 Taft Court. Suite 100, Rockville, MD 20850, USA
Tel: 301 340 8606
        1398
                                                                                        1458
                                                                                                                                                                       1518
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                                                                                                                                                                                                                                                         CTGAAGCTGAAGAGCTTGCTTTGACAAGTACACTGGGGAACACTTACCGAGTGGGTGACA 1578
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                                               371
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/clone_lib="Human placenta, large insert, pCMV expression
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                           GTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAAC
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                                                                                                                                                                                                                                                                                                                                                                552 CITATGAGCGTCCTAAAGACTCCATGATCTGGGGCTGTATCTGCATCCTGCGCGAG
      Email: CDRA@origene.com
This EST submission is part of an on-going human full-length
cloning project at Origene Technologies, Inc.
Please contact Origene for access.
Origene Technologies, Inc.
6 Taff Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seq primer: pCVV6 Sprime forward vector primer, OriGene
Technologies Inc.
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/mol_type="mRNA"
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/clone="TC124975"
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AUTHORS
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/db xref="taxon:9606"
/db xref="taxon:9606"
/db xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived_from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="cligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
from embryoid body outgrowths derived from hES cell lines
conditions."
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1 (bases 1 to 684)

1 standarder, Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

Lebkowski, J and Stanton, L.W.

Control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                        1339 GTCAGGCGCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGAGTCAAGCCAAGCCCG
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17000532625776 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
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  5; Indels
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Pax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rbrandenberger@geron.com
Insert Length: 684 Std Brror: 0.00.
Location/Qualifiers
    0; Mismatches
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Regenerative Medicine
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Matches 315; Conservative
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CN332332
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/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone_lib="GRN_EB" /clone_lib="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, 1
121- 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rbrandenberger@geron.com
Insert Length: 716 Std Error: 0.00.
Location/Qualifiers
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/db_xref="taxon:9606"
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ilarity 98.4%;
Conservative
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Matches 315; (
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CN332342
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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compatible end ligatio; Oligo-dr primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"
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/tfsue_type==mbryonic stem cells, embryoid bodies
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17000532295426 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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1 (bases 1 to 706)

Exandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fit Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
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Fax: 650 473 7760
                                                                                                                                                  18.8%; Score 312; DB 8; Lilarity 98.4%; Pred. No. 3.3e-78; Conservative 0; Mismatches 5;
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Insert Length: 706 Std Brror:
Location/Qualifiers
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Regenerative Medicine
Geron Corporation
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CN332335.1 GI:47332269
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CN332335
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from embryoid body outgrowths derived from hBS cell lines tl (p22), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
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/note="oligo dT primed, full-length enriched cDNA library
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1 (bases 1 to 716)

1 standards: Homo.

1 (bases 1 to 716)

1 in, X., Xu, C., Fang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

1 transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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                                                                                                                                                                                                                                                                               1459 GTAATGTGTTTGGTTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAAC
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17000533983768 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
CN332342
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                                                                                                                                                                Length 706
                                                                                                                                                                Score 312; DB 7; Length 70
Pred. No. 3.3e-78;
0; Mismatches 5; Indels
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BX473413

765 bp mRNA linear BST 04-SEP-2003
DKFZp686I15162_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686I15162_5', mRNA sequence.
                                                                                                                                               GTAATGTGTTTGTACTTGTATTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAAC 1518
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Bmail s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the CDNA
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Hominidae; Homo.

(Lobaca 1 to 765)

Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,

Well, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.

EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/clone="DKES086115162"
/dev stage="adult"
/lab_host="DH10B"
/clone 11b="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone (DKPZp686115162) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                             539 CTGAAGCTGAAGAGCTTGCTTTGACAAGTACACTGGGAAACACTTACCGAGTGGGTAC
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                                                                Length 751;
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                                                              Query Match 18.8%; Score 312; DB 1; L. Best Local Similarity 98.4%; Pred. No. 3.4e-78; Matches 315; Conservative 0; Mismatches 5;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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      cDNA-collection"
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Contact: MIPS
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DKFZp686P033_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686P033_S', mRNA sequence.
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  (p29), and H9 (p26) maintained in feeder-free
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/db_xref="taxon:9606"
/clone="DKRZp686P033"
/dev_arage="adult"
/lab_host="PH10B"
/clone lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Email 8.wiemann@dkfz- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No sl sequence available.
This clone (DKPZp686P033) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERWANY; Emall: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                   GTAATGTGTTGGTTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAAC
                                                                                                                                                                CTGAAGCTGAAGAGACTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACA
                                                                                                                            Gaps
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1 (bases 1 to 751)
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
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                                                                                   Length 716
                                                                                                                       5; Indels
                                                                               Score 312; DB 7;
Pred. No. 3.3e-78;
0; Mismatches 5;
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Unpublished (1999)
Contact: MIPS
MIPS
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H1 (p32), H7 conditions."
                                                                               Query Match
Best Local Similarity 98.4%;
Matches 315; Conservative
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1 (bases 1 to 7434)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., White, T.J., Sninsky, J., Adams M.D. and Cargill, M. Givello, D., White, T.J., Sninsky, J., Adams, M.D. and Cargill, M. A. Scan for Positively Selected Genes in the Genomes of Humans and
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Bubiar, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
  sites of the pCMVSPORT 6 vector. Library was normalized.
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This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                              563 CTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGAG
                                                                                                                                                                                                      GTAATGTGTTGGTTTGTACTTGTTATGGAAGCCCGAGGTTTTAACTGCGAAAGTAAAC
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Homo sapiens FN1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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                                                                     Length 911;
                                                                Score 312; DB 5; Length 91
Pred. No. 3.6e-78;
0; Mismatches 5; Indels
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/gene="FN1"
/locus_tag="HC8611"
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ilarity 98.4%;
Conservative
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Best Local (
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqrefégenoscope.cns.fr, web : www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecok V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX398838 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CS0D1065Y122 5-PRIME, mRNA sequence.
BX398838
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIOG5Y122"
/tissue_type="PLACENTA_COT_25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA_COT_25-NORMALIZED"
/note="Ist strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 911)

1 (bases 1 to 911)

1 (bases 2 to 911)

1 (bases 2 to 911)

1 (bases 3 to 911)

1 (bases 2 to 911)

On May 13, 2003 this sequence version replaced gi:30625651.
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                                                                     Length 765;
                                                                                                            Indels
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                                                                Score 312; DB 5;
Pred. No. 3.4e-78;
0; Mismatches 5;
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                                                              Query Match
Best Local Similarity 98.4%;
Matches 315; Conservative
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CTGAAGCTGAAGAGACTTGCTTTGACAGTACACTGGGAACACTTACCGAGTGGGTGACA 1578
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Harvesting a desired polypeptide produced by a recombinant host cell, for producing pharmaceuticals, comprises selecting a recombinant nucleic acid
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Factor Xa
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07-FEB-2003; 2003US-00360101.
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   Ad192189 Streptoki
Aar10194 Streptoki
Aar23120 Streptoki
Aay24794 Streptoco
Aaw94664 Streptoco
Aay01556 Native Bt
Aay90282 S. equisi
Aay24797 Streptoki
Aar11829 FB-FB-SK
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               GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                              - protein search, using frame_plus_n2p model
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AAY91829
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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The invention relates to a novel method for harvesting a (poly)peptide produced by a recombinant host cell. The novel method involves selecting a cell comprising a first nucleic acid encoding a leader peptide and a second nucleic acid fragment encoding the desired (poly)peptide. The first and second fragments are within the same open reading frame of the first nucleic acid and the leader peptide is functionally equivalent to The host cells and nucleic acids are useful for producing, harvesting and post-translational modification of polypeptides. The polypeptides may be used in the production of pharmaceuticals, e.g. as antigen for vaccine or immunogenic composition. This sequence represents a polypeptide relating to the novel method of the invention.
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nucleic acid fragments encoding a leader peptide and the
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TCCTCAATCGTCATCATGACAATGACATTTTTCCGTACGATTTTTACCAATGGATCAAGAG
                                          TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAATCTGGTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic gene encoding streptokinase - scale, high purity prodn. streptokinase used as a thrombolytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             streptokinase; thrombolytic agent; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uenoyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptokinase encoded by synthetic gene
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89JP-00307957.
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myocardial infarction.
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/note= "claim 1, 8

120. .352

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244. .414

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                                                                                                                                                                                         Streptokinase and its derivatives can be produced in large quantities with high purity for use as thrombolytic agents in patients with lung thrombus or myocardial infarction. See also AAR10195-R10200
                                                                                                                                                                                 GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGAAAGGCTTAAGTCCAAAATCA
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DNA encoding a polypeptide which binds to plasminogen and corresponds to region of streptokinase – useful to detect plasminogen in a sample and to treat myocardial infarction.

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AsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLysGly
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      Nucleic acid comprising a sequence encoding amino acids 14-414 of streptokinase, which binds to plasminogen and does not have a sequence comprising amino acids 60-414 is new. The polypeptide pref. comprises amino acids 244-352, 1-352, 120-352 or 244-414. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC
                                                                                                                                                                                          AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATTTACGTCCTTAAAAAGGG
                                                                                                                                                  ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT
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1322 1202 1262 340 360 induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCGTAGCGAACGTAAC AspValAspThrAsnGluLeuLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsn TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTACTACAATCTC GATGCTTTTGGTATTATGGACTATACCTTTAACTGGAAAAGTAGAGGATAATCACGATGAC Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; zSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis. present invention describes an isolated bacterial protein that Streptococcus equisimilis native streptokinase. Streptococcus dysgalactiae subsp. equisimilis.

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bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infaction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial althrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a degradation of fibr streptokinase at least one amino acid substitution that inactivates a degradation of the streptokinase at least two-fold. The present sequence represents native streptokinase at least two-fold. The present sequence standardise OS field)
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Sequence 414 AA

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Alignment Scor Pred. No.: Score: Percent Simila Best Local Sim Query Match:	Scores    milari   Simil	res: arity: milarity:	3.93e-178 1984.00 100.00\$ 100.00\$ 67.51\$	Length: Matches: Conservative: Mismatches: Indels: Gaps:	414 383 0 0 0	
US-09-940-	235	-10 (1-166	61) x AAY24794 (	(1-414)		
λ	183	ATTGCTGGA	CCTGAGTGGCTGCTA	GACCGTCCATCTGTCA	ACAACAGCCAATTGGTTGTT	242
ΩÞ	7	IleAlaGly	ProGluTrpLeuLeu			20
ò	243	AGCGTTGCT	GGTACTGTTGAGGG	ACGAATCAAGACATTA	GTCTTAAATTTTTTGAAATC	302
Db	21	ServalAla	GlyThrValGluGly	ThrAsnGlnAspileS		40
ò	303	GATCTAACA	TCACGACCTGCTCAT	GGAGGAAAGACAGAGC	AAGGCTTAAGTCCAAAATCA	362
ΩD	41	AspLeuThr	SerArgProAlaHis	GlyGlyLysThrGluG	AspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer	09
λō	363	AAACCATTT	GCTACTGATAGTGGC	GCGATGTCACATAAAC	AAACCATTTGCTACTGATAGTGGCGCGGATGTCACATAAACTTGAGAAAGCTGACTTACTA	422
Ωp	61	LysProPhe	AlaThrAspSerGly	AlaMetSerHisLysL		80
&	423	AAGGCTATT	CAAGAACAATTGATO	GCTAACGTCCACAGTA	ACGACGACTACTTTGAGGTC	482
Op	81	Lysalaile	GlnGluGlnLeuIle	AlaAsnValHisSerA	LysalailegingiugintenijealaasnvaltisserasnaspasptyrPhegiuval	100
ò	483	ATTĞATTTT	GCAAGCGATGCAACC	ATTACTGATCGAAACG	ATTGATTTTGCAAGGGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC	542
QQ	101	IleAspPhe	AlaSerAspAlaThr			120
ò	543	AAAGATGGT	TCGGTAACCTTGCCG	ACCCAACCTGTCCAAG	AATTTTGCTAAGCGGACAT	602
QQ	121	LysAspGly	ServalThrLeuPro	ThrGlnProvalGlnG		140
à	603	GTGCGCGTT	AGACCATATAAAGAA	AAACCAATACAAAACC	AAGCGAAATCTGTTGATGTG	662
QQ	141	ValArgVal	ArgProTyrLysGlu	LysProlleGlnAsnG	ValàrgValàrgProTyrLysGluLysProIleGlnAsnGlnAlaLysSerValàspVal	160
ò	663	GAATATACT	GTACAGTTTACTCCC	TTAAACCCTGATGACG	GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA	722
ΩP	161	GluTyrThr	ValGlnPheThrPro	LeuAsnProAspAspA	uspPheArgProGlyLeuLys	180
ά	723	GATACTAAG	CTATTGAAACACTA	GCTATCGGTGACACCA	TCACATCTCAAGAATTACTA	782
Db	181	AspThrLys	LeureurysThrreu	AlaileGlyAspThri	AspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeu	200
ò	783	GCTCAAGCA	CAAAGCATTTTAAAC	AAAACCACCCAGGCT	GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC	842
q <sub>Q</sub>	201	AlaGlnAla	GlnSerileLeuAsn	LysAsnHisProGlyT	yrThrileTyrGluArgAsp	220
È	843	TCCTCAATC	GTCACTCATGACAAT	GACATTTCCGTACGA	TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG	902
ΩÞ	221	SerSerlle	ValThrHisAspAsn			240

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                                                                                                                                                                                                                                                         Streptococcus equisimilis H46A, streptokinase, mutant, fibrinolytic, plasma clot, hydrolysis, haemolytic Streptococcus, plasminogen; plasmin, serine protease, fibrin; blood clot, thrombolytic, vascular thromboembolytic symptom; acute myocardial infarction;
TITACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAATCTGGTCTG
                                         AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG
                                                                                          GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                                          341 AspalaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAsp
                                                                                GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant streptokinase polypeptide - useful as plasmin-resistant thrombolytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus equisimilis native streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus dysgalactiae subsp. equisimilis
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                                    TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAATCTGGTCTG
                                                                     AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG
                                                                                                                   GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                                                                GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                                             AspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsn
                                                                                                                                                                                                             TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTACAACAATCTC
                                                                                   AsnGluGluIleAsnAsnThrAspLeuIleSerGluIysTyrTyrValLeuLysLysGly
                                                                                                                               ptide; streptokinase; streptokinase-specific antibody;
activity; thrombolytic therapy; glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptokinase-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus dysgalactiae subsp. equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Native streptokinase protein sequence
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                   The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence represents native SK. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPIg) to hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                  ATTGCTGGACCTGATGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT
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Streptokinase; SX; hybrid plasminogen activator; fibrin binding region;
                        GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                               GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                          Thrasnarg11e11eThrVa1TyrMetGlyLysArgProGluGlyGluAsnalaSerTyr
    261 AsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrValLeuLysLysGly
                                   GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThr11eLysTyrVa1
                                                                                                       TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
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Yadav M;
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and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (P1) comprising an epptiope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. Pl is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                               AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC
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and Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin. This sequence represents the human Streptococcus equisimilus streptokinase protein sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, fibrin binding regions of human fibronectin, which are from fibrin binding of mains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a ; > Sundaram Nihalani D,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical
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pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG: The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of aardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 12-SSP-2003 to standardise OS field)
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composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising a daministering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaccutical composition comprising a blood clots in patients with a thrombosi condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a streptokinase at least two-fold. The present sequence represents a streptokinase at least two-fold. The present sequence represents a streptokinase and maltose binding protein fusion protein
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## Sequence 795 AA

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Mismatches: 0 Indels: 0 Gaps: 0	(1-795)	ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT 	AGCGTTGCTGGTACTGTTGAGGGGACGAACQAAGATTTTGAAATTTTTTGAAATCTTAATTTTTGAAATCTTTTTTGAAATCTTTTTTGAAATCTTTTTTGAAATCTTTTTTGAAATCTTTTTTTGAAATCTTTTTTTT	GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGAAGGGTTAAGTCCAAAATCA 	AAACCATTTGCTACTGATAGTGGGGGATGTCACATAAACTTGAGAAAGCTGACTTACTA 	AAGGCTAITCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC 	ATTGATTTTGCAAGGGATGGAACGATTACTGAACGGAAGGGGAAGGTCTACTTTGCTGAC 	AAAGATGGTTCGGTAACCTTGCCGACCCACCTGTCCAAGAATTTTTGCTAAGGGGACAT 	GTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAAGCGAAATCTGTTGATGTG 	GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGGTCTGAAA 	GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
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& 8	1263	ACCAP       Thras	ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGCTA	
& g	1323	CATTI       Histe	CATTTAGCC 1331          HisLeuala 764	
RESULT AAR1182 ID AA XX AC AA	LT 9 1829 AAR11829 AAR11829;	stand	dard; protein; 531 AA.	
i t X t	08-JUL-1991	991		
e z z z i	Fibrin-binding Streptokinase;		on conjugate. g protein; fibrinolysis; intravascular thrombi; fibrinogen; ;; fusion protein.	ä
8 8	Staphylococcus	coccus	s aureus.	
žett	Key Peptide		Location/Qualifiers 261 /label= FB monomer	
4444	Peptide Peptide		62119 /label= FB monomer 120531 /label= streptokinase	
ž & ;	501168	6-A.		
(윤)	-APR-1	991.		
≨ ‰ X	-NOV-1	1686	89US-00437769.	
£ X	-SEP-1	987;	B7US-00099242.	
g X	REA-)	REATI	CREATIVE BIOMOLEC.	

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                                                                                                             TTTACTTACCGGGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG
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SerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu
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                                                                                         Imparting injectable fibrinolytic agent - with affinity for intravascular thrombus, by linking agent to fibrin binding domain.
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                                                                                                                                                                               The conjugate comprises an FB-FB dimer linked to streptokinase The FB fragment has selective affinity for fibrin, low affinity for fibrinogen, and minimal immunogenicity, imparting thrombus- targetting capability. See also AAK11821 and AAK11828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGCTGGACCTGATGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT
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Mismatches:
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                                                                                                                                                Disclosure, Fig 5, 18pp; English
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Modified forms of streptokinase resistant to enzymatic cleavage - useful as thrombolytic agents in treating thrombosis and in medical equipment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the wild type plasminogen-binding fragment of streptokinase. This fragment was used in the design of a modified streptokinase has an in vitro degradation rate at least 2 times slower
                                                                                                                                                                                                                                                                                                    361 ThrasnargileileThrValTyrMetGlyLysArgProGluGlyGluAsnalaSerTyr
                                         TITACTIACCGIGITAAAAATCGGGAACAAGCITATAGGATCAAIAAAAAATCTGGICTG
                                                                                            AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAGGG
                                                                                                                                              GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                                                             GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                                                                                                                   TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
                                                                                                                                                                                                                                                                   Plasminogen-binding fragment; streptokinase; degradation; MBP; thrombolytic agent; blood clot; bolus; maltose-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wild type plasminogen-binding fragement of Streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus dysgalactiae subsp. equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 12-13; 65pp; English.
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                                             The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the ProS8-Lys55-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence is mutant SK K59E. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPlg) to plasmin (HPlm), which is a serine protease able to catalyse the hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen
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Matches:
Conservative:
Mismatches:
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                        Claim 4; Col 11-14; 17pp; English
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DB:
thrombolytic agent
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Modified forms of streptokinase resistant to enzymatic cleavage - useful as thrombolytic agents in treating thrombosis and in medical equipment.
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                                                                                                                                                                                                                                                                                                                                                               AspalaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAsp
                            GAAAAGCCGTATGATCCCTTTTGATCGCAGTCACTTGAAACTGTTCACCCATCAAATACGTT
                                                  280 GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrlleLysTyrVal
                                                                                                             GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                   TTAGACTICAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTACAACAATCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasminogen-binding fragment; streptokinase; degradation; MBP; thrombolytic agent; blood clot; bolus; maltose-binding protein
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/label= Maltose_binding_protein
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382. .1194
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than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of U/kg, opt. as a bolus rather than by continuous infusion. (Updated of OCT-2003 to standardise OS field)
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Matches:
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Best Local Similarity:
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The invention relates to a method for identifying and quantifying one or more proteins in complex mixtures by selectively isolating peptides not containing histidine nor arginine (NRNR peptides) from each protein, and determining the relative concentration of one or more proteins in different samples from the ratio between the areas of estimated theoretical spectra for each NRNR peptide labeled with different isotopes in each sample. The method comprises: (a) enzymatically or chemically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying and quantifying proteins in complex mixtures by selectively isolating peptides not containing histidine nor arginine from each protein, and determining the relative concentration of proteins in
                                          TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACTCTC
                                                                                          LeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeu
                                                                                                           GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
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DORTA-DUQUE J F D C.
PEREZ V A B.
VALDES J G.
LOPEZ L J G.
PEYT R P.
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                                                                                                                                                                                                     different samples.
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                                                                                                                                                                                                                                       GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGCAAGGCTTAAGTCCAAAATCA
                                                                                                                                                                                                                                                                              AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA
                                                                                                                                                                                                                                                                                                                     AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC
                                                                                                                                                                                                                                                                                                                              ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
                                                                                                                                                                                                                                                                                                                                                                      AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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 vivo in a mammal, preferably at a dose of 20000 U/kg, optionally as
bolus rather than by continuous infusion. (Updated on 17-OCT-2003 to
standardise OS field)
                                                                   1194
382
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1
                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                   2.6e-176
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99.74%
66.91%
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Best Local Similarity:
                                       Sequence 1194 AA,
                                                          Alignment Scores:
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hydrolyzing the sample or samples of proteins; (b) chemically modifying alpha and epsilon amino groups (alpha- and epsilon-NH2) of every peptide obtained in step (a); (c) isolating the NRNR peptides by cation exchange chromatography from the mixture of peptides obtained in step (b); (d) identifying proteins by mass spectrometry analysis of the NHNR peptides obtained in step (c); (e) differential isotopic labeling of proteins camples previously to step (a) or during steps (a) or (b) and immediately mixing at least a portion of the samples; and (f) relative quantifying of mixing at least a portion of the samples; and (f) relative quantifying of areas of estimated theoretical spectra of the pair of NHNR peptides identified in step (d), as well as from the ratio between the areas of the estimated theoretical spectra of fragments from the NHNR peptides. Generated in step (d). Also described is a kit for the identification and quantification of proteins in complex mixtures, which comprises the method and kit are useful for identifying or diagnostic uses, in complex mixtures. The present sequence represents a streptorianse protein, which is used in an example from the present
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## Sequence 415 AA;

Alignment Scores:			
Pred. No.:	3.79e-176	Length:	415
Score:	1963.00	Matches:	379
Percent Similarity:	896.86	Conservative:	1
Best Local Similarity:	98.70%	Mismatches:	4
Query Match:	86.79	Indels:	0
DB:	6	Gaps:	0
(314 t) 36460ddx - (1331-1) 01-366-040-00-811	20 A COCIOR - 117	(1 416)	

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CTGAATGAAGAAATAAACAACACCTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAA 1019
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                                                                                                               ValAspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArg 320
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                                                                                  GluPheThrTyrHisValLysAsnArgGluGlnAlaTyrGluIleAsnLysLysSerGly 260
                                                                                                                                                                                                                                                                    GGGGBAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATAC
                                                                                                                                                                               GITGATGTCGATACCAACGAATTGCTAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGT
                                                                  GAGTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAATCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell; immunogenicity; immune system; SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus dysgalactiae subsp. equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-immunogenic; epitope; T-cell; immunogen
immunogl bulin; therapeutic; streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptokinase (SK) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                         AAW86143 standard; protein; 414 AA.
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97GB-00016197.
97GB-00025270.
97US-0067235P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98GB-00007751
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                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOV-) BIOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-045301/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-1997;
31-JUL-1997;
28-NOV-1997;
02-DEC-1997;
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03-MAR-1999
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Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of given species.

Example 6; Fig 28; 77pp; English.

proteins. The relations of machine and the analysin of sequence of the protein; (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate at reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of the SK protein. (Updated on 17-OCT-2003 to standardise OS field) invention relates to a method for the production of non-immunogenic 

Sequence 414 AA;

414 1378 100 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.12e-175 1958.00 98.96% 98.69% 66.62% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Score: Query Match: DB:

(1-414)US-09-940-235-10 (1-1661) x AAW86143

422 482 542 GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA 362 100 AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT 602 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 722 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 782 9 80 20 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT 1 lleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal 41 AspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer **AAGGCTATTCAAGAACAATTGATCGCTAAACGTCCACAGTAACGACGACTACTTTGAGGTC** 183 303 363 423 483 543 191 663 723 ò 셤 셤 Š ઠે 셤 ઠે 셤 8 % 8 셤 8 요 ò B ઠ 셤 ઠે

1022 1082 1142 1202 1262 380 220 902 962 260 280 300 320 340 360 Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug; vaccine; carrier; diagnosis; therapy; complement; C3; CVF; plasminogen; streptokinase; fibrin; blood clot; thrombolysis; plasmin; GCTCAAGCACAAAGCATTTTAAACAAAACCACCCAGGCTATACGATTTTATGAACGTGAC TCCTCAATCGTCACCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG TITACTTACCGIGITAAAAATCGGGAACAAGCITATAGGATCAATAAAAAATCTGGTCTG **AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG** AsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLysGly GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC Wild type streptokinase from Streptococcus equisimilis. Streptococcus dysgalactiae subsp. equisimilis ö Carter Ą. Hamilton AA, AAB01295 standard; protein; 414 98GB-00026925. (revised)
(first entry) CATTTAGCC 1331 HisLeuAla 383 myocardial infarction. (BIOV-) BIOVATION LTD. Carr FJ, Adair FS, WPI; 2000-423372/36 WO200034317-A2 08-DEC-1998; 02-FEB-1999; 12-SEP-2003 25-SEP-2000 15-JUN-2000. 281 301 381 783 201 843 221 903 241 963 261 1023 1083 1143 1263 1203 1323 AAB01295; AAB01295 쉼 q ò 원 δ ద ò g ò 셤 Š 셤 g 셤 셤 ò ò ð ò

Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes.

Example 2; Fig 5; 42pp; English

proteins or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at least one of these T cell epitopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for producing a protein with an enzymatic activity which has a beneficial therapeutic effect, a protein used to convert inactive daugs to its active form within a living organism, a vaccine, a protein used as a carrier of other molecules or a protein which binds to other molecules within or introduced within the living organism in order to alter the bio distribution of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic protein is useful in medicine, diagnosis and in manufacture of a therapeutic or a diagnostic agent. Streptokinase is produced by certain strains of beta-haemolytic agent. Streptokinase is produced by certain strains of beta-haemolytic considerable clinical importance owing to its ability to efficiently bind human plasminogen, potentiating its activation to plasmin and thereby consort thrombosis, improving survival and preserving left ventricular function following myocardial infarction. The new method colds Streptokinase is an effective thrombolytic agent in the treatment of consory thrombosis, improving survival and preserving left ventricular communogenic and the production of fleting antibodies in humans communogenic and the production of neutralising antibodies in humans proving a lower a lower of the wild type streptokinase. The new method could proving all infarctions of the wild type streptokinase. The altered streptokinase sequence is given in AAB01296. See GENESEQ records AAB01289-B01302. (Updated on 12-2003 to standardise OS field)

Sequence 414 AA;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1.12e-175 1958.00 98.96% 98.69% 66.62% Best Local Similarity: Query Match: DB: Score: Percent Similarity: Alignment Scores: Pred. No.:

US-09-940-235-10 (1-1661) x AAB01295 (1-414)

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qq	141	ValArgValArgProTyrLysGluLysProIleGlnAsnGlnAlaLysSerValAspVal 160
Š	663	GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGCTCTAAA 722
g	161	GlufyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGlyLeuLys 180
δ	723	GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACCATCTCAAGAATTACTA 782
ф	181	AspThrIysheuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeu 200
ò	783	GCTCAAGCACAAAGCATTTTAAAAAAAAACACCCCAGGCTATACGATTTATGAACGTGAC 842
qq	201	AlaGlnAlaGlnSerlleLeuAsnLysThrHisProGlyTyrThrIleTyrGluArgAsp 220
ò	843	TCCTCAATCGTCACTCATGACAATGACATTITCCGTACGATTTTACCAATGGATCAAGAG 902
QQ	221	SerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu 240
ò	903	TITACITACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 962
Dβ	241	PheThrTyrHisValLysAsnArgGluGlnAlaTyrGluIleAsnLysLysSerGlyLeu 260
ò	963	AATGAAGAATAAACAATGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG 1022
ΩÞ	261	AsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysGly 280
ò	1023	GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 1082
ОР	281	GlulysProTyrAspProPheAspArgSsrHisLeuLysLeuPheThrIleLysTyrVal 300
ò	1083	GATGTCGATACCAACGAATTGCTAAAAAGTGAGCTCTTTAACAGCTAGCGAACGTAAC 1142
Ор	301	AspValAsnThrAsnGluLeuLeuLeuLysSerGluGlnLeuLeuLeuThrAlaSerGluArgAsn 320
ઠે	1143	TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTACAACAATCTC 1202
ΩP	321	LeuaspPheargaspLeuTyraspProargaspLysalaLysLeuLeuTyrasnasnLeu 340
ò	1203	GAIGCITITIGIATIAIGGACTATACCITIAACIGGAAAAGTAGAGGATAATCACGAIGAC 1262
qq	341	AspalaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAsp 360
ò	1263	ACCAACCGTATCATAACCGTTTATATGGGCAAGGACCCGAAGGAGAGAGA
qq	361	ThrAsnArglleIleThrValTyrMetGlyLysArgProGluGlyGluAsnAlaSerTyr 380
ò	1323	CATTTAGCC 1331
qq	381	HistenAla 383

Search completed: January 28, 2006, 02:08:17 Job time : 132.543 secs

Title: Perfect score:

Sequence:

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Scoring table:

Searched:

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    Sequence 264, Application US/10360101
    Patent No. 6861236
    Patent No. 6861236
    ABENERAL INFORMATION:
    APPLICANT: Moll, Gert N.
    APPLICANT: Leenhouts, Cornelis J.
    APPLICANT: Leenhout Export and modification of (poly)peptide in the lantibiotic way
    PILR REPERENCE: 2183-5673

                                                                                                                                                      Sequence 12, Appl Sequence 12, Appl Sequence 4, Appl Sequence 4, Appl Sequence 2, Appl Sequence 3, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 6, Appl Sequ
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Sequence 16
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Sequence 1
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US-08-488-940-18

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US-09-294-457-12

US-09-919-703-12

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US-09-919-703-12

US-09-658-179-1

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CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: BP 02077060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: PatentIn version 3.1
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ORGANISM: Artificial Sequence
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US-10-360-101-264
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LENGTH: 413
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-1.0=/cgn2_1/USPTO_ippo_n0del - DEV-xlp
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Patent No. 5240845
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1: /cgn2_6/ptOdata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptOdata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptOdata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptOdata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptOdata/1/iaa/RB_COMB.pep:*

6: /cgn2_6/ptOdata/1/iaa/RB_COMB.pep:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                protein search, using frame_plus_n2p model
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US-07-854-5968-19

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Patent No. 6210667
GENERAL INFORMATION:
APPLICANT: Reed, GUY L.
TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMBERG & SUNSTEIN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT
                                                                                                                                                                                                                              ADDRESSER: BROWBERG & SUNSTEIN, LLP
STREET: 125 Summer Street
CITY: Boston
STATE: Massachusetts
CONTRY: USA
ZIP: 0210
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION: 1653
PRIOR APPLICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Strimpel, Harriet M.
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
TELEROOMER/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/ASSISSERIES/A
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Best Local Similarity:
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; FILING DATE: 06-JUL-1990 ; SEQ ID NO:1: ; LENGTH: 414 5240845-1 Alignment Scores:	183	243 AGCGTTGCTGGTACTGTTGAGGGACGAATCAAGACATTAGTCTTAAATTTTTGAAATC  [	ON 41 ASPECUIASSET STATEMENTS OF THE STATEMENT OF THE STATEMENT STATEMENT OF THE STATEMENT STATE	Qy         423 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACGACTACTTGAGGTC         482	Qy         483 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAAGCGCAAGGTCTACTTTGCTGAC         542	Qy         543 AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT         602	Qy         603 GTGCGCGTTAGACCATATAAAGAAAAACCAAAACCAAGCGAAATCTGTTGATGTG         662	Qy         663 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGTCTCAAA         722	Qy         723 GATACTAAGCTATTGAAAACACTAGGTATCGGTGACACCATCACATCTCAAGAATTACTA 782	Oy 783 GCTCAAGCACAATTTTAAACAAAACCACCCCAGGCTATACGATTTATGAACGTGAC 842 	Qy         843 TCCTCAATGGTCACTCATGACAATGTTTTTCCGTACGATTTTACCAATGGATCAAGA         902	903 241 963	Qy 1023 GABABGCGTATGATCGCTTTGATCGCAGTCACTTGAACTGTCACCATCAATACGTT 1082
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Gaps: 0  -09-940-235-10 (1-1661) x US-08-560-098A-52 (1-440) 	Maccattaccarraccarraccarraccarraccaraaccrracacaaaccractacta	543 AAAGATGCTTGCCGACCCACCTGTCCAAGATTTTTGCTAAGCGCACT	187 GlufyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGlyLeuLys 2 723 GATACTAAGCTATGAAAACACTAGCTATCGGTCACCATCACATCTCAAGAATTACTA 7 723 GATACTAAGCTATTGAAAACACTAGCTATCGGTCACCATCACATCTCAAGAATTACTA 7 207 ASpThrLysLeuLeuLysThrLeuAla11eGlyAspThr11eThrSerGlnGluLeuLeu 2 783 GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATAGATTATGAACGTAC 8 783 GCTCAAGCATATTAAACAAAAACAATATTACAGATTATTAGACGTAC 8 843 TCCTCAAATCGTCACTCATGACAATTTTCCGTACGATTTTACCAATGGATCAAGAG 9 [	247 8 903 7 267 1 963 D 287 D 1023 G	1083 327 1143 347 1203
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281 GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal 30 1083 GATGTCGATACCAACTAATGCTAAAAGTGAGCGAGCTCTTAACAGCTAGCGAACGTAAC 1083 GATGTCGATACCAACTAATGCTAAAAGTGAGCTAACAGCTAGCGAACGTAAC 11 301 AspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsn 32 1143 TAGACTTCAGAGATTTATAACGATCCTCGTGATAAGGCTAAACTACTCTACAATGTC 12 1111	hrAsnArgileileThrValTyrMetGlyLysArgProGluGlyGluAsnAlaSe ATTTAGCC 1331            sheuAla 383. 52 Application US/08560098A 76841 RMATION:	APPLICANT: WNENDT, Stephan APPLICANT: HEINZEL-WIELAND, Regina APPLICANT: STEPFENS, Gred Josef TITLE OF INVENTION: Proteins having Fibrinolytic and TITLE OF INVENTION: Coagulation-inhibiting Properties NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: ADDRESSE: Evenson, McKeown, Edwards & Lenahan STRET: 1200 G Street, N.W., Suite 700 STATE: DC	COMPUTER READABLE FORM:  COMPUTER READABLE FORM:  COMPUTER PER FLORM:  COMPUTER: IBM PC COMPATIBLE  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  CURRENT APPLICATION DATA:  PFLICATION NUMBER: US/08/560,098A  PRIOR APPLICATION DATA:  PRIOR APPLICATION NUMBER: P 44 40 892.7		### TODOLGSY: linear

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; Sequence 3, Application US/08488940
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APPLICANT: Reed, Guy L.

TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMBERG & SUNSTEIN, LLP
STREET: 1.2 Summer Street
CITY: Boston
STATE: Massachusetts
CONNEX: USA
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MEDIUM TYPE: Ploppy disk
COMPUTER: PROPPY disk
COMPUTER: PROPPY disk
COMPUTER: DISP Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFICATION NUMBER: 60/69,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Strimpel, Harriet M.
REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMUNICATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 amino acids
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Matches:
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MOLECULE TYPE: protein
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Best Local Similarity:
Query Match:
DB:
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Fatent No. 5854049
GENERAL INFORMATION:
TITLE OF INVENTION:
CORRESPONDENCES: 20
CORRESPONDENCES: 20
CORRESPONDENCE Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FULL OF INVENTION:
FULL OF INVENTION:
FULL OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE:
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Conservative:
Mismatches:
Indels:
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MOLECULE TYPE: protein
US-08-488-940-3
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Best Local Similarity:
Query Match:
DB:
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                      TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: Floppy disk
COMPUTER: BM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FLING DATE: 03-JUN-1992
CLASSIPICATION: 435
ATTOMEY/AGENT INPORMATION:
NAME: MCDONNEIL JOHN J
REGISTRATION NUMBER: 26,949
REPRENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPRAK: 312-715-1034
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-854-596B-26; Sequence 26, Application US/07854596B; Patent No. 5434073; GENERAL INFORMATION:
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CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                        REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
RESERENCE NUMBER: 05433/00901
TELEPRONE: 617/542-5070
TELEPRONE: 617/542-8906
TELER: 200154
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
LENGTH: 1194 amino acids
STRANDEDMESS: not relevant
TOPOLOGY: linear
                                            APPLICATION NUMBER: US/08/488,940 FILING DATE: 09-UNN-1995 CLASSIFICATION: 514 ATTORNEY AGENT INFORMATION: NAME: Fraser, Janis K.
                                                                                                                                                                                                                                                                                                                                                                                           7.01e-184
1966.50
99.74%
66.91%
                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
OPERATING SYSTEM:
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Best Local Similarity:
Query Match:
DB:
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261 LeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLys 280
                                                                                              CICGAIGCTTTIGGIATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAAATCACGAT
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                                         281 GlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyr
                                                                                GTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: US-JUN-1992
CLASSIFICATION: 435
ATTONEY/AGENT INPORMATION:
NAME: MCDORNEJ, John J
REGISTRATION NUMBER: 26,949
REBRENCE/DOCKET NUMBER: 26,949
REBRENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELERAK: 312-115-1034
TELERAK: 312-115-1234
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Matches:
Conservative:
Mismatches:
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Dr. John J. McDonnell
Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity:
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CITY: Chicago
STATE: IL
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Mismatches:
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Matches:
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66.79%
TELEX: 910-221-5317
INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-854-596B-26
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Query Match:
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Qy         1203 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1262           Db         362 AspAlaPhedlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsp 381           Qy         1263 ACCAACCGTATCATAACGGCAAGGGAAGGAGAAATGCTAGTAT 1322           Db         382 ThrAsnArg1	S-07-854-5968-15 Sequence 15, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION: APPLICANT: Dawson, Keith M APPLICANT: Czaplewski, Lloyd G TITLE OF INVENTION: Proteins and NUMBER OF SEQUENCES: 73 CORRESPONDENCE 173 CORRESPONDENCE DT. JOHN J. McDonnell STREET: Ten South Wacker Drive, CITY: Chicago STRATE: IL COUNTRY: USA ZIP: 66666 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPATE: REDIUM TYPE: READABLE FORM: REDIUM TYPE: READABLE FORM: REDIUM TYPE: READABLE FORM: REDIUM TYPE: READABLE FORM: REDIUM TYPE: IBM PC COMPATE: REDIUM TYPE: IBM PC C	APPLICATION NUMBER: US/07/854,596B    PILING DATE: 03-JUN-1992   CLASSIFICATION: 435   ATTORNEY/AGRY INFORMATION:   NAME: McDonnell, John J   REGISTRATION NUMBER: 26,949   REFRENCE/DOCKET NUMBER: 92,337   TELECOMMUNICATION INFORMATION:   TELECOMMUNICATION INFORMATION:   TELECOMMUNICATION INFORMATION:   TELECOMMUNICATION INFORMATION:   TELECOMMUNICATION INFORMATION:   TELEFROME: 312-715-1000   TELEFROME: 3110-1000   TELEFROME: 312-715-1000   TELEFROME: 312-715-1000   TELEFROME: 312-715-1000   TELEFROME: 312-715-1000   TELEFROME: 312-	Alignment Scores:  Pred. No.: 1958.00  Matches: Score: Score: 98.96\$ Conservative: 1 Best Local Similarity: 98.96\$ Conservative: 1 Best Local Similarity: 98.64  Query Match: 66.62\$ Indels: 0  US-09-940-235-10 (1-1661) x US-07-854-596B-15 (1-440)  Qy 183 ATTGCTGGACCTGGTGCTGCTAGACCGTCCATTGGTTGTT 242
Query Match:         66.62%         Indels:         0           DB:         1         Gaps:         0           US-09-940-235-10 (1-1661)         x US-07-854-596B-19 (1-435)         (1-435)           Qy         183 ATTGCTGGACCTGAGGGGGGCTGCTAGACCGTCCATCTGACAACAGCCAATTGGTTGTT         242           Db         22 IleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal 41           Qy         243 AGCTTGCTGGTACTGTTGAGGGACGAATCAAGACATTAGTAAATTTTTGAAATC         302           Db         42 SerValAlaGlyProGluGYMPrValGluGYMPrAnGlashGalaGagaatCaattagtagtagtagtagtagtagtagtagtagtagtagt	303 GATCTAGCAACCTGCTCATGAGGAAGACAGGCAAGGCTAAGTCCAAAATCA 303 GATCTAACATCACGACCTGCTCATGAGGAAGACAGGCTTAAGTCCAAAATCA 62 AspleuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer 363 AAACCATTGCTACTGATGGGGGGATGTCACATAACTTGAGAAGCTGACTTACTA 423 AAGCATTCATACATGATGGGCGCATGTCACATAACTTGAGAAGCTGACTTACTA 423 AAGCATTCAAGAACAATTGATGGTGGCGATGTCACATAACTTGAGAAGTTACTTAC	162 663 182 202 202 222 243 903	

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TOPOLOGY:
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Matches:
Conservative:
Mismatches:
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ZIP: 66666
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-940-235-10 (1-1661) x US-07-854-596B-43 (1-483)
                                                                                                                nucleic acids
                                                                      APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OP INVENTION: Proteins and nucleic acid
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
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Sequence 43, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDONNEIL, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .34e-183
                                                       APPLICANT: Dawson, Keith M APPLICANT: Hunter, Michael
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98.96%
98.69%
66.62%
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SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-07-854-596B-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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CITY: Chicago
STATE: IL
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDORNell, John J
REGISTRATION NUMBER: 26,949
REBERENCE/POCKET NUMBER: 26,949
REBERENCE/POCKET NUMBER: 26,949
TELECOMMUNICATION INFORMATION:
TELEFRAK: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                     483
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14
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                            TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    3.34e-183
1958.00
98.96%
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                                                                                                                                                                                                                                                                                         LENGTH: 483 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                        US-07-854-596B-47
                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                           GTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
                                                                         GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
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Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Dawson. Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATTTAGCC 1331
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266 AspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeu 285
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                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                  Indels:
              TELEPHONE: 312-715-1000
TELERAX: 312-715-1024
TELEX: 910-221-5317
INPORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acids
     FELECOMMUNICATION INFORMATION
                                                                                                                                                                3.38e-183
1958.00
98.96%
98.69%
66.62%
                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                           US-07-854-596B-28
                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                  126
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                                                 TCCTCAATCGTCACTCATGACATTTTTCCGTACGATTTTACCAATGGATCAAGAG
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                                    GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dawson, Keith M
APPLICANT: Dawson, Keith M
APPLICANT: Dawson, Keith M
APPLICANT: Hunter Michael G
APPLICANT: Gazplewaki, iloyd G
ITTLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCES: 73
CORRESPONDENCES: 73
CORRESPONDENCES: 73
CORRESPONDENCES: 73
CORRESPONDENCES: 73
CONTRY: USA
ZITY: Chicago
STATE: IL
COUNTRY: USA
ZITY: Chicago
STATE: IL
COUNTRY: USA
ZITY: Chicago
STATE: IL
COMPUTER: FIADPY disk
COMPUTER: FIADPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
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; Patent No. 5434073
; GENERAL INFORMATION:
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NAME: MCDONNEII, JOHN J
REGISTRATION NUMBER: 26, 349
REFERENCE/DOCKET NUMBER: 92, 337
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  378
               Conservative:
Mismatches:
Indels:
                                                                                  US-09-940-235-10 (1-1661) x US-07-854-596B-35 (1-859)
    Matches:
1958.00
98.96%
98.69%
66.62%
           Percent Similarity:
Best Local Similarity:
Query Match:
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CONDERSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
GITY: Chicago
STATE: 11
COUNTRY: USA
ZIP: 60606
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT IRPORMATION:
NAME: MCDONNELL JOHN J
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
REGISTRATION INFORMATION:
TELEFONDE: 312-715-1000
TELEFONDE: 312-715-1000
TELEFONDE: 312-715-1000
TELEFONDE: GOOD OF SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 8959 amino acids
TURNOTALION POR SEQ ID NO: 35:
LENGTH: 8959 amino acids
TURNOTALION POR SEQ ID NO: 35:
TELEGTH: SHOPEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Caplewaki, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION:
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US-07-854-596B-35
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Pred. No.:
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                                                                                                                                                                                                                                                                                              STREET: 215 Franklin Street
CITY: Boston
STATE: M4
COUNTR: M4
COUNTR: M5
CONPUTER: M2A
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patchtin Release #1.0, Version #1.30
SOFTWARE: Patchtin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-JUN 1995
CLASSIFICATION NUMBER: US/08/488,940
ATTORNEY/AGRNT INFORMATION:
NAME: Frader, Janis K.
REGEREROLOSCET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: A17/542-5070
                                                                                                                                                                                                   Sequence 17, Application US/08488940
Patent No. 5854049
GENERAL INFORTION:
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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Matches:
Conservative:
Mismatches:
Indels:
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
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Pred. No.:
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Search completed: January 28, 2006, 02:41:17 Job time : 42.6951 secs

on:

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Sequence 264, Application US/10360101
Sequence 264, Application No. US20040009550A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way FILE REPERENCE: 2103-6673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT PILING DATE: 2003-02-07
PRIOR FILING DATE: 2002-05-24
PRIOR FILING DATE: 2002-05-24
NUMBER: PAGE ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 264
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52634, A
4, Appli
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94, Appl
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-MODEL=frame+ n2p.model -DEV=xlp

-Q=/Cqn2 1/05F0 spool py U305940235/runat 27012006 144219 27635/app query.fasta_1.7708
-Q=/Cqn2 1/05F0 spool py U305940235/runat 27012006 144219 27635/app query.fasta_1.7708
-DB=Published Applications AA Main -QFWT=fastan -SÜFFIX=rapbm -MINMĀTCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL_OUTFMT=pto -NORM=ext -HRAPSISE=500 -MINLEN=0
-MAXLEN=200000000 -USER=U309940235 @CGN 1 1 805_@runat 27012006 144219 27635
-NCPU=6 -ICPD=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOČK=100
-LONGLOG -DEV_TIMEOŪT=120 -WARN_TIMEOŪT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 2, Appli
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                                                                                                                                                   January 28, 2006, 01:51:16; Search time 108.622 Seconds (without alignments) 12778.538 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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US-10-300-215-252
US-10-300-215-253
US-09-919-703-12
US-10-474-792-658
US-09-940-235-4
US-10-171-311-64
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Copyright (c) 1993 - 2006
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                                                                                                                                                                                         Sequence 1, Application US/10988943

Publication No. US20050176085A1

GENERAL INPORMATION:

APPLICANT: Center for Genetic Engineering and Biotechnology

TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE

TITLE OF INVENTION: COMPLEX MIXTURES.

TITLE OF INVENTION: COMPLEX MIXTURES.

FILE REFERENCE: Proteomics CL0003-269

CURRENT APPLICATION NUMBER: US/10/988,943

CURRENT APPLICATION NUMBER: US/10/988,943

SUFFMER PATILING DATE: 2004-11-15

SEQ ID NOS: 61

SEQ ID NOS: 61

SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Streptococcus equisimilis
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HisLeuAla 383
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US-10-988-943-1
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Alignment Scores:

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       Matches:
Conservative:
Mismatches:
Indels:
                                                      US-09-940-235-10 (1-1661) x US-10-988-943-1 (1-415)
 Length:
                                       Gaps:
1.06e-177
1963.00
98.96%
98.70%
66.79%
              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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482 100 542 120 602 140

662 160 722 200

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902 240 962 260

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1203 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1262
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             AAACCATTTGCTACTGATAGTGGCGCGGTGTCACATAAACTTGAGAAAGCTGACTTACTA
                                                               423 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC
                                                                             GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
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US-10-300-215-253
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 25. Application US/10300215

Publication No. US20030153043A1

GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
APPLICANT: ADAIR, Fiona Suzamne
APPLICANT: ADAIR, Fiona Suzamne
APPLICANT: ADAIR, Fiona Suzamne
APPLICANT: ADAIR, FIONA SUZAMNE
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
TITLE OF INVENTION: MON-IMMUNGENIC PROTEINS
FILE REFERENCE: MER-104-Con.1
CURRENT FILING DATE: 1099-11-20
PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
PRIOR PILING DATE: 1999-11-10
PRIOR PLING DATE: 1997-05-21
PRIOR PLING DATE: 1997-05-21
PRIOR PLING DATE: 1997-05-21
PRIOR PLING DATE: 1997-07-31
PRIOR PLING DATE: 1997-11-28
PRIOR PLING DATE: 1997-11-28
PRIOR PLING DATE: 1998-04-14
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Best Local Similarity:
Query Match:
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US-10-300-215-252
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Pred. No.:
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; Patent No. US20020165129A1
; GENERAL INFORMATION:
; APPLICANT: RADAIN. Simon W.
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate;
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate;
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate;
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate;
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate;
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate;
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate;
; PRIOR REPLICATION NUMBER: US 09/294,457
; PRIOR PILING DATE: 1999-04-19
; PRIOR PILING DATE: 1999-04-19
; PRIOR PILING DATE: 1995-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PASSESEQ for Windows Version 4.0
; SEQ ID NO 12
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Matches:
Conservative:
Mismatches:
Indels:
                  APPLICANT: CARK, FIGICIS JUSSEDII
APPLICANT: ADAIR, FIONS SUZADNE
APPLICANT: HAMILTON, ANICA ADNE
APPLICANT: HAMILTON, ANICA ADNE
APPLICANT: HAMILTON, ANICA ADNE
APPLICANT: HAMILTON, ANICA ADNE
APPLICANT: HAMILTON, MICHAE
TITLE OF INVENTION: NON-IMMUNCERIC PROTEINS
FILE REFERENCE: MER-104-COn.)
CURRENT APPLICATION NUMBER: US 09/438,136
FRIOR PRIOR APPLICATION NUMBER: US 09/438,136
PRIOR PILING DATE: 1999-11-10
PRIOR PELICATION NUMBER: GB 9710480.6
PRIOR PLILING DATE: 1997-05-21
PRIOR PELING DATE: 1997-05-21
PRIOR PELING DATE: 1997-05-31
PRIOR PELING DATE: 1997-05-31
PRIOR PELING DATE: 1997-11-28
PRIOR PELING DATE: 1998-04-14
PRIOR PELING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 254

SEQ ID NO 253
LENGTH: 414

LENGTH: AT4
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1947.00
98.69%
98.17%
66.25%
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Best Local Similarity:
Query Match:
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| Publication No. US20040236072A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Olmsted, Stephen
| APPLICANT: Nickbarg, Elliot
| APPLICANT: Winter, Lourie
| TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
| FILE REFERENCE: AM 100399 | CURRENT FILING DATE: 2003-10-14 |
| CURRENT FILING DATE: 2003-10-14 |
| NUMBER OF SEQ ID NOS: 674 |
| SOFTWARE: PatentIn version 3.0
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Conservative:
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TYPE: PRT
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Matches:
Conservative:
Mismatches:
Indels:
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-12
                                                                                                                              Gaps:
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1928.00
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TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEIN:
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT FILING DATE: 1099-12-23
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR APPLICATION NUMBER: 10 3825/DEL/98
PRIOR APPLICATION NUMBER: 10 3825/DEL/98
PRIOR PILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 259
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Sequence 64, Application US/10171311

GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yanei
APPLICANT: Monahan, John
APPLICANT: Materia, Shubhangi
APPLICANT: Materia, Shubhangi
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
TITLE OF INVENTION: OF CERVICAL CANCER
TITLE OF INVENTION WHEBER: US/10/171,311
CURRENT APPLICATION NUMBER: US 60/298,159
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Matches:
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APPLICANT: Kumar, Rajesh; APPLICANT: Sahni, Girish; APPLICANT: Rajagopal, Kammara; APPLICANT: Nihalani, Deepak; APPLICANT: Sundaram, Vasudha; APPLICANT: Sundaram, Vasudha; APPLICANT: Yadav, Mahavir
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Sequence 70. Application US/10236031B
Sequence 70. WS20030219760A1
Sequence 70. WS20030219760A1
Sequence 70. WS20030219760A1
Sequence 70. WS20030219760A1
SPLICANT: Grains, Reven R.
APPLICANT: Gullans, Steven R.
APPLICANT: Bueno, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic Tests
FILE REFERENCE: B00801/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236,031B
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR PRINTOR DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
SEQ ID NO 70
SEQ ID NO 70
LENGTH: 2328
                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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          PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-10-14
PRIOR PILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 2328
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PRIOR FILING DATE: 2001-06-13
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CRGANISM: Homo sapiens
US-10-171-311-64
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ORGANISM: Homo sapiens
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US-10-236-031B-70
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Alignment Scores:

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| Sequence 98, Application US/10374979
| Publication No. U320030219793A1
| GENERAL INFORMATION:
| APPLICANT: John P. Carulli et al.
| TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
| FILE REFERENCE: 032796-021
| CURRENT PELLING DATE: 2003-03-04
| PRIOR PPLICATION NUMBER: US/09/44,398
| PRIOR FILING DATE: 2000-04-05
| PRIOR FILING DATE: 2000-04-05
| PRIOR PLILING DATE: 1999-01-13
| PRIOR PLILING DATE: 1999-01-13
| PRIOR FILING DATE: 1999-01-13
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ORGANISM: Homo sapiens
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Publication No. US20040221326A1

GENERAL INFORMATION:
APPLICANT: Babij, Philip
APPLICANT: Bodine, Peter Van Nest
TILLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
FILE REFERENCE: 102796-212
CURRENT APPLICATION NUMBER: US/10/477,238A
CURRENT FILING DATE: 2003-10-10
FRIOR APPLICATION NUMBER: US 60/290,071
FRIOR APPLICATION NUMBER: US 60/291,311
FRIOR APPLICATION NUMBER: US 60/391,313
FRIOR PELING DATE: 2000-05-17
FRIOR PELING DATE: 2000-02-17
FRIOR PELING DATE: 2000-03-04
FRIOR APPLICATION NUMBER: US 60/361,293
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US-10-477-238A-677
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US-10-182-936A-98

J Sequence 98, Application US/10182936A

Publication No. US20040038860A1

GENERAL INFORMATION:
APPLICANT: Anisowicz, Anthony
APPLICANT: Anisowicz, Anthony
APPLICANT: Danagnez, Veronique
APPLICANT: Danagnez, Veronique
APPLICANT: Reagents and Method for Modulating DKK-Mediated Interactions
TITLE OF INVANTION: Reagents and Method for Modulating DKK-Mediated Interactions
TITLE OF INVANTION: Reagents and Method for Modulating DKK-Mediated Interactions
FILE REPERBENCE: 032796-143
CURRENT APPLICATION NUMBER: US/10/182,936A

PRIOR PELING DATE: 2002-08-02

PRIOR PELING DATE: 2002-06-17

PRIOR APPLICATION NUMBER: US 60/291,311

PRIOR PELING DATE: 2002-05-17

PRIOR PELING DATE: 2002-05-01

PRIOR PELING DATE: 2002-03-04

PRIOR PELING DATE: 2002-03-04
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; ORGANISM: Homb sapiens
US-10-182-936A-98
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                                                                     Sequence 677, Application US/10680287A

Publication No. US20040244069A1

GENERAL INFORMATION:

APPLICANT: Babi; Philip

APPLICANT: Babi; Frederick J. III

APPLICANT: Beck, Frederick J. III

APPLICANT: Beck, Frederick J. III

APPLICANT: Beck, Frederick J. III

APPLICANT: Bodine, Peter Van Nest

TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation

FILE REFERENCE: 2003-10-08

FRICA PLICATION NUMBER: US/10/680,287A

CURRENT FILING DATE: 2002-05-13

PRIOR APPLICATION NUMBER: US 60/290,071

PRIOR PRICATION NUMBER: US 60/291,311

PRIOR PELICATION NUMBER: US 60/291,311

PRIOR PELICATION NUMBER: US 60/391,293

PRIOR PLING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: US 60/361,293

PRIOR APPLICATION NUMBER: US 60/361,293

PRIOR PELING DATE: 2002-03-04

PRIOR PELING DATE: 2002-03-04

NUMBER OF SEQ ID NOS: 812

SOFTWARE: FasteSEQ for Windows Version 4.0

SEQ ID NO 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
DB:
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                                               RESULT 14
US-10-680-287A-677
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US-10-680-287A-677
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US-10-477-173-677
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Pred. No.:
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Sequence 677, Application US/10477173 Publication No. US20050070699A1 GENERAL INFORMATION:

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APPLICANT: Allen, Kristina M. APPLICANT: Allen, Kristina M. APPLICANT: Allen, Kristina M. APPLICANT: Manales, Arturo J. APPLICANT: Morales, Arturo J. APPLICANT: Morales, Arturo J. APPLICANT: Masswicz, Anthony APPLICANT: Liu, Wei Mes R. APPLICANT: Liu, Wei Mes R. APPLICANT: Liu, Wei J. APPLICANT: DATE: 203-11-10 CURENT PILING DATE: 2001-05-11 PRIOR APPLICANT: NUMBER: US 60/290,071 PRIOR PILING DATE: 2001-05-17 PRIOR FILING DATE: 2001-05-17 PRIOR FILING DATE: 2002-02-02 PRIOR PILING DATE: 2002-02-04 PRIOR PILING DATE: 2002-03-04 PRIOR PILING DATE: 2002-03-04 NUMBER: US 60/361,293 PRIOR FILING DATE: 2002-03-04 NUMBER: PastSEQ for Windows Version 4.0
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Genome Therapeutics Corporation and
Allen, Kristina M.
Yaworsky, Paul
Morales, Arturo J.
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Job time : 128.622 secs
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ORGANISM: Homo sapiens
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Best Local Similarity:
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634, App 30, Appli 4, Appli 7, Appli 3, Appli 13, Appl

11, Appl 1008, Ap 7, Appli 319, App 7, Appli 140, App

OM nucleic

Run on:

Sequence:

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Sequence 2, Application US/10631558
| Sequence 2, Application US/10631558
| Sequence 2, Application No. US200526059841
| GENERAL INFORMATION:
| APPLICANT: Kumar, Rajesh
| APPLICANT: Rajespa, Kammara |
| APPLICANT: Rajespa, Kammara |
| APPLICANT: Rajespa, Mahavi, Deepak |
| APPLICANT: Sundaram, Vasudha |
| FILLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID |
| FILLE REFERENCE: 07064-009002 |
| CURRENT FILLNG DATE: 2003-07-11 |
| PRIOR APPLICATION NUMBER: US/09/940,235 |
| PRIOR FILLNG DATE: 1999-12-23 |
| PRIOR FILLNG DATE: 1999-12-24 |
| NUMBER OF SEQ ID NOS: 28 |
| SEQ ID NO 2 |
| LENGTHA: 414 |
| LENGTHA: A14 |
| LENGTHA: A14
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US-10-995-561-628

US-10-995-561-632

US-10-995-561-634

US-11-095-561-634

US-11-095-561-634

US-11-013-759-7

US-11-013-759-7

US-11-013-759-13

US-11-013-759-13

US-11-013-759-13

US-11-013-759-13

US-11-013-759-11

US-11-052-554A-8

US-11-052-554A-260

US-11-115-639-33

US-11-115-639-33
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US-11-077-550-82
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Command line parameters:
-0A0DEL=Frame+ n.2p.model -DEV=xlp
-0=/cgn2 1/USFTO spool p/US09940235/runat 27012006 144220 27676/app_query.fasta_1.7708
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR_MAX=100
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-MAXLEN=200000000 -USRE-US09940235 GCGN 1 1 0 erunat 27012006 144220 27676
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                                                                                                     January 28, 2006, 02:09:11; Search time 4.80939 Seconds (without alignments) 7479.985 Million cell updates/sec
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Sequence 622
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1: /cgn2 6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
2: /cgn2 6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
3: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
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5: /cgn2 6/ptodata/2/pubpaa/USO3 NEW PUB.pep:*
6: /cgn2 6/ptodata/2/pubpaa/USO3 NEW PUB.pep:*
7: /cgn2 6/ptodata/2/pubpaa/USO3 NEW PUB.pep:*
8: /cgn2 6/ptodata/2/pubpaa/USO3 NEW PUB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                         protein search, using frame_plus_n2p model
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US-10-631-558-4
US-11-006-119-31
US-10-995-561-631
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Perfect score:
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Result

Minimum DB Maximum DB

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                                                         GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA 362
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         GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCOMMATION;
GENERAL INCOMMATION;
APPLICANT: Krystald, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Deptides and Their Use to Ameliorate
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/003005
CURRENT APPLICATION NUMBER: US/11/032,951
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR PILING DATE: 1999-04-19
PRIOR PLING DATE: 1999-04-19
PRIOR PLING DATE: 1999-04-19
PRIOR PLING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 413
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377
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic polypeptide
                                                                                                                      US-11-032-951-12; Sequence 12, Application US/11032951; Publication No. US20050282741A1; GENERAL INFORMATION:
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1928.00
98.95%
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                                                                                   CATTTAGCC 1331
                                                                                             Percent Similarity:
Best Local Similarity:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
                                                 US-09-940-235-10 (1-1661) x US-10-631-558-2 (1-414)
                                    Gaps:
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APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEIN
FILE OF INVENTION NUMBER: US/09/940,235
CURRENT FILING DATE: 109/940,235
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR PELLOR DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 4
LENGTH: 259
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; Sequence 31, Application US/11006119
; Sequence 31, Application US/11006119
; Publication No. US20050260691A1
; GENERAL INFORMATION:
    APPLICANT: Ward, Brian
; APPLICANT: Caffrey, Rebecca
; APPLICANT: Caffrey, Rebecca
; APPLICANT: Li, Hongshan
; APPLICANT: Podust, Vladimir
; APPLICANT: Podust, Vladimir
; APPLICANT: Podust, Vladimir
; APPLICANT: Ciphergen Biosystems, Inc.
; TITLE OF INVENTION: Serum Biomarkers for Chagas Disease
; FILE REPERENCE: 016866-012130US
; CURRENT APPLICATION NUMBER: US/11/006,119
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Matches:
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Pred. No.:
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US-10-631-558-4
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   ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGCCAAGGTCTACTTTGCTGAC
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Publication No. US20050260598A1
GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Najagopal, Kammara
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1461 AATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCT 1520
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Publication No. US20050272054A1
GENERAL INFORMATION:
TOTAL INFORMATION:
TITLE OF INVENTION: CENEDICANE DISCREES AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: CENEDICANE DISCREES AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THERROF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NO 622
LENGTH: 657
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                                   Mismatches:
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US-10-995-561-622
                  Percent Similarity:
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US-10-995-561-622
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| Publication No. US20050272054A1
| GENERAL INPORMATION:
| APPLICANT: CARGILL, Michele et al. |
| TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF |
| TITLE OF INVENTION: US/10/995, 561 |
| TITLE OF INVENTION: US/10/995, 561 |
| CURRENT APPLICATION NUMBER: US/10/995, 561 |
| CURRENT FILING DATE: 2004-11-24 |
| NUMBER OF SEQ ID NOS: 85702 |
| SOFTWARE: PSELSEQ for Windows Version 4.0 |
| SEQ ID NO 631 |
| LENGTH: 642
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CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: US 60/527,153
PRIOR FILING DATE: 2003-12-05
PRIOR FILING DATE: 2003-12-05
PRIOR FILING DATE: 2004-04-22
PRIOR FILING DATE: 2004-04-26
PRIOR FILING DATE: 2004-04-26
PRIOR FILING DATE: 2004-11-06
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 31
LENGTH: 300
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ORGANISM: Homo sapiens
US-10-995-561-631
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US-10-995-561-631
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                                                                                                                                                                       Sequence 629, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: CARDIOVACULAR DISORDERS AND DRUG RESPONSE, METHODS (TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL010159

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILLING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly
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US-10-995-561-633
Sequence 633, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
                                                                                                     1641 AGAATAAGCTGTACCATC 1658
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; ORGANISM: Homo sapiens
US-10-995-561-629
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Best Local Similarity:
Query Match:
DB:
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US-10-995-561-629
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFRENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER: OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 633
LENGTH: 2296
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Sequence 623, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVAGCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DATE: 2004-11-24
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NOS: 85702
SEQ ID NO 623
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; ORGANISM: Homo sapiens
US-10-995-561-633
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; ORGANISM: Homo sapiens
US-10-995-561-623
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1581 TATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGG 1640
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| Publication No. US20050255114A1
| GENERAL INPORMATION:
| APPLICANT: Labat, Ivan
| APPLICANT: Stache-Crain, Birgit
| APPLICANT: Tang, Y. Tom
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INVENTION: WIGHER: US/10/404-07 |
| PRIOR APPLICATION NUMBER: US 60/462,047 |
| PRIOR APPLICATION NUMBER: US 60/462,047 |
| NUMBER OF SEQ ID NOS: 1704 |
| SOFTWARE: pt SEQ_genes Version 1.0 |
| SEQ ID NO 1545
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ORGANISM: Homo sapiens
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Bublication No. US20050272054A1

GENERAL INFORMATION:

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DAPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 627

LENOTH: 2355

TYPE: PRT
                                                                                                                                 | TATGAGGGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGG 1640
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US-10-995-561-627
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US-10-995-561-627
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US-10-995-561-621

Sequence 621, Application US/10995561

Sequence 621, Application US/10995561

Sequence 621, Application No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FSSISEQ for Windows Version 4.0

SEQ ID NO 621

LENGTH: 1341
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TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOOISS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 626
LENGTH: 2386
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; ORGANISM: Homo sapiens
US-10-995-561-621
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Query Match:
DB:
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Best Local Similarity:
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US-10-995-561-626
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1043 GluTyrThrlleTyrVallleAlaLeuLysAsnAsnGlnLysSerGluProLeulleGly 1062
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1218 LysTrpAspArgGlnGlyGluAsnGlyGlnMetMetSerCysThrCysLeuGlyAsnGly 1237
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1178 ArgMetSerGluSerGlyPheLysLeuLeuCysGlnCysLeuGlyPheGlySerGlyHis 1197
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
KURRENT FILING DATE: 200411-24
NUMBER OF SEQ ID NOS: 85702
GAGTTTACTTACCGTGTT------AAAATCGGGAACAAGCTTATAGGATC-----
                                                          945 AATAAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATAT
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1063 ArgLysLysThrGly---GlnGluAlaLeuSerGlnThrThrIle-------
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1119 ArgGlyAlaThrTyrAsnIleIleValGluAlaLeuLysAspGlnGlnArgHisLysVal
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1139 ArgGluGluValThrValGlyAsnSerValAsn---GluGlyLeuAsnGlnProThr
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Publication No. US20050272054A1
GENERAL INFORMATION:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 625 LENGTH: 1259
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Best Local Similarity:
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| S52 ValValValSerGlyLeuMetValAlaThrLysTyrGluValSerValTyrAlaLeuLys
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92CAAAGCATTTTAAACAAAAACCACCCA	28 ATTTATGAACGTGACTCCTCAATCGTCACTGACAATGACATTTCCGTACGATT 884            :: 10 lleLysTyrGluLysProGlySerProProArgGluVal 1022	85 TTACCAATGGATCAA	00 GAGTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATC 944    :::	45 AATAAAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATAT 1004        :::          :::::     ::: 63 ArgLysLysThrGlyGlnGluAlaLeuSerGlnThrThrIIe 1076		65 TTCACCATCAAATACGTTGATGTCGAAGGAATTGCTAAAAAGTGAGCAGCTCTTA 1124        ::    :::     ::: 83AspThrSerGluTyrIleIleSerCysHisProVal 1094	n n	SS CTACTCTACAACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTA 1244              12 AlaThrieuThrGlyLeuThr 1118	45 GAGGATAATCACGATGACACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGGA 1304	GGAGAGAATGCTAACATTTAGCCGGTGGTGGTCAGGCGCAGCAAATGGTTCAG    ::    ::: ArgGlyAlaThrTyrAsnIleIleValGluAlaLeuLysAsgGlnClnArgHisLys	52 CCCGAGTCCCCGGTGGCTGTCAAAGCAAGCCCGGTTGTTATGACAATGGAAAACAC 1421 	22 TATCAGATAAATCAACAGTGGGGGGCCTACCTAGGTAATGTGTTGGTTTGTACT 1478    :::    :::::	99 TGTTATGGAGGAGGCCGAGGTTTTAACTGCGAAAGTAAACCTGAAGCTGAAGACCT 1535 		GACTCCATGATCTGGGACTGTACCTGCATCGGGCTGGGCGAGGG 1640	
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Search completed: January 28, 2006, 02:57:52 Job time: 26.8094 secs

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Scoring table:

Searched:

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A;Residues: 1-410 cML>
A;Cross-references: UNIPROT:P00779; UNIPARC:UP1000002BE73; GB:X72832; NID:g407876; PIDN
A;Experimental source: strain H46A
C;Genetics:
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C;Species: Streptococcus "equisimilis"
C;Species: Streptococcus "equisimilis"
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A22801
R;Malke, H; Roe, B; Ferretti, J.J.
R;Malke, H; Roe, B; Ferretti, J.J.
A;Title: Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis ]
A;Reference number: A22801; MUID:85232082; PMID:2989113
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C,Superfamily: streptokinase
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Query Match:
                                 A; Molecule type: DNA
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=CGD2_1/USFTO.po.model -DEV=xlp
-Q=CGD2_1/USFTO.po.model -DEV=xlp
-Q=CGD2_1/USFTO.po.model -DEV=xlp
-DB=PIR -QFWT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62 -TRAMS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USFR=US09940235 @CGN_1 1 185 @vunat_27012006 144218 27578 -NCPU=6 -ICPU=3
-NO NWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-PEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                       protein search, using frame_plus_n2p model
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Score

No. Result

Database

us-09-940-235-10.rpr

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	423 AAGGCTATTCAAGAACAATTGATGGTAACGT 	483 ATTGATTTTGCAAGCGATGCAACCATTACTGA 	543 AAAGAIGGITCGGIAACCITGCCGACCCAACC 	603 GTGCGCGTTAGACCATATAAAGAAAAACCAAT) 	663 GAATATACTGTACAGTTTACTCCCTTAAACCC 	723 GATACTAAGCTATTGAAAACACTAGCTATCGG 	783 GCTCAAGCACATTTTAAACAAAAACCACACAAAAACCAAAAAACCAAAAAA		843 TCCTCAATCGTCACTCATGACAATGACATTTT0	903 TITACTTACCGTGTTAAAAATCGGGAACAAGC	963 AATGAAGAAATAAACAACACTGACCTGATCTC	287 AsnGluGluileAsnAsnThrAspLeuileSe	1023 GAAAAGCCGTATGATCCTTTGATCGCAGTCA(	1083 GATGTCGATACCAACGAATTGCTAAAAAGTGA 	1143 TTAGACTTCAGAGATTTATACGATCCTCGTGA	347 LeudspPheArgAspLeuTyrAspProArgAsi		367 AspAlaPheGlyIleMetAspTyrThrLeuTh			1323 CATTTAGCC 1331           407 HisLeuala 409	
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21, 6620-6625, 1982
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umber: A00967; MUID:83127125; PMID:6760891
A00967
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ences: UNIPROT:P00779; UNIPARC:UPI0000172BF5
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(EC 3.4.-.-) - Streptococcus sp.
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r-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004
%00967
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	663 GAATATCTGTACAGTTACTCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 72	843 TCCTCAATCGTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGGG 90	Db   327 AspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuThrAlaSerGluArgAsn 346
221 SerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuDrOMetAspGlnGlu 240 903 TTTACTTACGTTAAAAATCGGGAACAGGCTTATAGGATCAATAAAAAATCTGGTCTG 241 PheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeu 260 963 AATGAAGAATAAACAACTGACCTGATCTCTGAGAAATATACGTCCTTAAAAAA 101 261 A8nGluGluIleAsnAsnThrAspLeuIleSerLeuGluTyrLysTyrValLeuLysLys 280 1020 GGGGAAAAGCCGTATGATCCTTTGATCGACTCATTGAAATATTACGTCCTTAAAAAA 107 281 GlyGluLysProTyrAspProPheAspArgGatCACTTGAACACTTGAACACTTGAACACTTGATGATCTCACAACAACACGAACCT 113 281 GlyGluLysProTyrAspProPheAspArgGatCACTTGAACACTTAACAGCTAGCGAACGT 113 301 ValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArg 320 1140 AACTTCAGAGATTTATACGATCCTCGTGATAACACTAACAACTAAT 119 125 AATGAACTTCAGAGATTTATACGATCCTCGTGATAAACTACTCTACAACAAT 119 111	Oy         1200 CTCGATGGTTTTGGTATTATGGACTATACCTTAACTGGAAAGTAGAGGATAATCACGAT 1259           Db         341 LeuAspAlaPheGly1leMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAsp 360           Cy         1260 GACACCAACCGTATAATCGCTTATATGGCCAAGCGACCCGAAGGAATGCTAGC 1319           Db         361 AspThrAsnArgIleIleThrValTyrMetClyLysArgProGluGlyGluAsnAlaSer 380           Cy         1320 TATCATTTAGCC 1331           Db         381 TyrHisLeuAla 384	S02723 Streptochinase G precursor - Streptococcus sp. (strain 19908) C.Species: Streptococcus sp. C.Species: Streptococcus sp. C.Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004 C.Accession: S02723 R.Malter, F.; Siegel, M.; Malke, H. Nucleic Acids Res. 17, 1262, 1989 A.Title: Nucleotide sequence of the streptokinase gene from a group-G Streptococcus. A.Accession: S02723; MUD:89160265; PMID:2922269 A.Accession: S02723 A.Molecule type: DNA A.Residues: 1-440 < WALD A.Genetics: A.Gene	Alignment Scores:  Pred. No.:  1942.00  Matches: 375  Score: 1942.00  Matches: 375  Percent Similarity: 98.43*  Conservative: 2  Best Local Similarity: 97.91* Mismatches: 66.08*  Indels: 0  Gaps: 0  183 ATTGCTGGACCTGACTGCTCACACCTCCTCTCAACACACCCAATTGGTTGTT  Db

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streptokinase - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A43867; JUD292
R;Ohkuni, H.; Todome, Y.; Suzuki, H.; Mizuse, M.; Kotani, N.; Horiuchi, K.; Shikama, N.;
Infect. Immun. 60, 278-283, 1992
A;Title: Immunochemical studies and complete amino acid sequence of the streptokinase fr
A;Reference number: A43867; MUID:92104686; PMID:1370275
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A,Residues: 1-414 <OHK>
A,Cross-references: UNIPROT:Q57391; UNIPARC:UPI0000175C82
A,Experimental source: M type 12 strain A374
A,Note: sequence extracted from NCBI backbone (NCBIP:74592)
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84.60%
56.92%
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streptokinase A precursor - Streptococcus pyogenes (strain SF130/13)
C;Species: Streptococcus pyogenes
C;Date: 18-0ct-1989 #sequence_revision 18-0ct-1989 #text_change 09-Jul-2004
C;Accession: S02724
R;Walter, F; Siegel, M.; Malke, H.
Nucleic, Acids Rss. 17, 1261, 1989
A;Title: Nucleotide sequence of the streptokinase gene from a Streptococcus pyogenes typ.
A;Reference number: S02724
A;Reference number: S02724
A;Accession: S02724
A;Accession: S02724
A;Accession: S02724
A;Cross-references: UNIPROT:P10520; UNIPARC:UP1000017021D; EMBL:X13399; NID:g47435; PIDN
C;Genetics:
A;Gene: ska
C;Superfamily: streptokinase
F;1-26/Domain: signal sequence #status predicted <SIG>F;27-440/Product: streptokinase #status predicted <MAT>
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C;Species: Streptococcus pyogenes
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S04168
R;Huang, T.T.; Malke, H.; Ferretti, J.J.
Mol. Microbiol. 3, 197-205, 1989
A;Itle: The streptokinase gene of group A streptococci: cloning, expression in Escheria. Reference number: S04168; MUID:89343623; PMID:2668686
A;Rocession: S04168
A;Molecule type: DNA
A;Wolecule type: DNA
A;Residues: 1-440 cHUA>
A;Rosidues: 1-440 cHUA>
A;Conetics:
C;Genetics:
A;Gene: ska
C;Superfamily: streptokinase
C;Superfamily: streptokinase
F;1-26/Domain: signal sequence #status predicted cMIT>
F;27-440/Product: streptokinase A #status predicted cMAT>
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streptokinase A precursor - Streptococcus pyogenes (strain NZ131)

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J. Biol. Chem. 261, 2113-2116, 1986

A;Title: Evolution of the fibronectin gene.
A;Reference number: A26284; MUID:86111901; PMID:3003095
A;Accession: A26284
A;Molecule type: DNA
A;Residues: 1447-1540 oLDb
A;Cross-references: UNIPARC:UPI0000112E37; GB:M12549; NID:g182688
A;Note: the authors translated the codon TTC for residue 1494 as Glu
R;Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
A;Title: Sequence analysis and in vivo expression show that alternative splicing of ED-A;Reference number: S00848; MUID:88233940; PMID:337563
A;Accession: S03917
A;Molecule type: DNA
A;Residues: 1594-1767, VV, 1769-1783 <PAO>
A;Cross-references: UNIPARC:UF1000017432B; EMBL:X07718; NID:g31402
A;Cross-references: UNIPARC:UF1000017432B; EMBL:X07718; NID:g31402
A;Cross-references: UNIPARC:UF1000017432B; EMBL:X07718; NID:g31402
A;Note: the authors translated the codon AAC for residue 1631 as Asp
R;Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986
A: Title: Design and Acceptor splice signals within an exon of the human fibronectin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Title: Donor and acceptor splice signals within an exon of the human fibronectin gene A.Reference number: A24854; MUID:87030929; PMID:3770201
A.Accession: A24884
A.Accession: A24884
A.Accession: A24884
A.Residues: 1992-2147 < VIB>
A.Cross-references: UNIPARC:UPI000017432C; GB:X04530; NID:g31436
B.Gutman, A.; Yamada, R.M.; Kornblihtt, A.
BEBS Lett. 207, 145-148, 1986
A.Title: Human fibronectin is synthesized as a pre-propolypeptide.
A.Reference number: A24476; MUID:87030890; PMID:3770189
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A; Accession: A27.

A; Accession: A27.

A; Accession: A28.

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Accession: A27.

A; T75-1759, 1885

B; MUD: 8284965; PMID: 2992939

A; Accession: A91008

A; Cross-references: UNIPARC: UP1000017432E; UNIPARC: UP1000017432E; GB: X02761

R; Kornblihtt, A.R.; Vibe-Pedersen, K. Baralle, F. B.

Nucleic Acids Res. 12, 5853-5868, 1984

A; Accession: A93529; WUID: 84272258; PMID: 6462919

A; Accession: A93529; WUID: 84272258; PMID: 6462919
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A; Residues: 1434-1537 <OL2>
A; Crose-references: UNIPARC: UPI0000174331; GB: K00055; NID: g182680; PIDN: AAA52459.1; PID
R; Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
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A; Residues: 1594-2386 - BER>
A; Residues: 1594-2386 - BER>
A; Cross-references: UNIPARC: UPI000016A928; GB:M10905; NID:G182696; PIDN:AAA52462.1; PID
R; Umezawa, K.; Kornblihtt, A.R.; Baralle, F.E.
R; Umezawa, K.; Kornblihtt, A.R.; Baralle, F.E.
R; ERBS Lett. 186, 31-34, 1985
A; Title: Isolation and characterization of CDNA clones for human liver fibronectin.
A; Reference number: A22245; MUID:85231203; PMID:2989004
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A; Residues: 973-2080;2112-2386 <RO2>
A; Cross-references: UNIPARC; UPI00001742F; UNIPARC; UPI0000174330; GB:X00739
R; Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10133-10196; 1983
A; Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell
A; Reference number: A21011; MUID:83290929; PMID:6688418
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A;Accession: S77671
A;Status: translation not shown
A;Molecule: translation not shown
A;Molecule: type: DNA
A;Residues: 1-128 <KAP>
A;Cross-references: UNIPARC:UPI000000562; EMBL:UZ5853; NID:g818908; PIDN:AA85729.1; PI
A;Note: allele 2
A;Accession: S77672
A;Status: translation not shown
A;Molecule: type: DNA
A;Residues: 1-128 <KAZ>
A;Cross-references: UNIPARC:UPI0000000562; EMBL:UZ5854; NID:g818910; PIDN:AA865730.1; PI
A;Note: allele 3
A;Note: allele 3
C;Genetics:
A;Gene: stain E2/M3
C;Genetics:
A;Gene: stain B2/M3
C;Genetics:
A;Genetics:
A;Genetic
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NyAlternate names: fibronectin splice form ED-A
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiAccession: A2446; A26284; G39317; A24854; A24476; A91008; A93529; A21011; A90495; A22
Ribean, D.C.; Bowlus, C.L.; Bourgeois, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A;Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A;Reference number: A26460; MUID:8717578; PMID:3031656
A;Reference number: A26460
A;Reference number: A26460
A;Residues: 1-49 cDBA
A;Residues: 1-49 cDBA
A;Residues: 1-49 cDBA
A;Residues: L49 cDBA
A;Residues: L40 cDBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 722
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Characterization of a 31,000-dal

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C, Comment: The extra domain and connecting strand 3 are subject to developmental and tis
C, Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
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A;Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C;Superfamily: fibronectin type I repeat homology; fibronectin type II repeat homology;
C;Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicat
F;1-26/Domain: signal sequence #status predicted <SIG>
                                                 A,Title: Human plasma fibronectin. Demonstration of structural differences between the A,Reference number: $14357; MUID:91190085; PMID:2012601
A,Accession: $14357
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 2071-2080;2112-2356 <GAR4>
A;Cross-references: UNIPARC:UP1000017433C; UNIPARC:UP1000017433D
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F;52-272/Domain: fibrin and heparin binding <FHB>
F;52-87/Domain: fibronectin type I repeat homology <1F1>
F;97-135/Domain: fibronectin type I repeat homology <1F2>
F;141-179/Domain: fibronectin type I repeat homology <1F2>
F;186-225/Domain: fibronectin type I repeat homology <1F3>
F;231-270/Domain: fibronectin type I repeat homology <1F4>
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A;Residues: 1614-1630, T',1722-2081,2113-2244 <TRE>
A;Residues: 1614-1630, T',1722-2081,2113-2244 <TRE>
A;Cross-references: UNIPARC:UP100001433B
R;Garcia-Pardo, A.; Pearlstein, B.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A;Title: Primary structure of human plasma fibronectin.
A;Reference number: A23891; MUID:85261459; PMID:4019516
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                      274, 731-738, 1991
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Best Local Similarity:
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A Accession 1201
A; Cross-references: UNIPARC:UPI00000046A; GB:M27589; NID:g182705; PIDN:AAA52465.1; PID: A; Accession: B22245
A; Molecule type: mRNA
A; Residues: 1975-1991;2017-2039 < UM2>
A; Cross-references: UNIPARC:UPI0000014332; UNIPARC:UPI0000174333; GB:M27590
R; Sekiguchi, K.; Klos, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A; Title: Human liver fibronectin complementary DNAs: identification of two different mes A; Reference number: 152394; MUID:87026578; PMID:3021206
A; Accession: 165273
A; Scatus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 < SEK>
A; Cross-references: UNIPARC:UPI00006E04C; GB:M14060; NID:g182701; PIDN:AAA52464.1; PID: R; Kornblihtt, A.R.; Vibe-Pedersen, K.; Barralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A; Title: Isolation and characterization of CDNA clones for human and bovine fibronectine A; Reference number: A21165; MUID:83221567; PMID:6304699
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                                                                                                                                                                                                                                                                                                                                repeat homology <1F7>
repeat homology <1F8>
repeat homology <1F9>
F;308-608/Domain: collagen binding <CBR.*
7;308-32/Domain: fibronectin type I repeat homology <1F6-F;360-401/Domain: fibronectin type II repeat homology <2F1 F;420-461/Domain: fibronectin type II repeat homology <2F2 F;470-508/Domain: fibronectin type I repeat homology <1F7-F;518-555/Domain: fibronectin type I repeat homology <1F7-F;518-559/Domain: fibronectin type I repeat homology <1F8-F;518-559/Domain: fibronectin type I repeat homology <1F8-F;518-559/Domain: fibronectin type I repeat homology <1F8-F761-599/Domain: fibronectin type I repeat homology <1F8-
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Mismatches:
Indels:
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Matches:
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F;2085-2124/Domain: fibronectin type I repeat homology <1F10>
F;2130-2167/Domain: fibronectin type I repeat homology <1F11>
F;2130-2167/Domain: fibronectin type I repeat homology <1F11>
F;2130-2167/Domain: fibronectin type I repeat homology <1F11>
F;214-209/Domain: fibronectin type I repeat homology <1F11>
F;11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;216-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,302-
F;215-2167,2174-2200,2198-2209/Disulfide bonds: #status predicted
F;399,497,511,846,976,1213,1987/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;1205,1692/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;2246/Disulfide bonds: interchain (to 2250) #status predicted
F;2250/Disulfide bonds: interchain (to 2260) #status predicted
F;2250/Disulfide bonds: interchain (to 2260) #status experimental
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A; Residues: 1-2477 < HTM>
A; Residues: 1-2477 < HTM>
A; Residues: 1-2477 < HTM>
A; Cross-references: UNIPARC: UNIPARC: UPI000012A7C6; EMBL: X15906; NID: 956163; PID: R; Schwarzbauer, J.B.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A; Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript. A; Reference number: $12455; MUID: 88054951; PMID: 2445560
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A;Cross references: UNIPARC:UP10000177ARA; EMBL:X15906
A;Cross references: UNIPARC:UP10000177ARA; EMBL:X15906
A;Tamkun, J.W.; Schwarzbauer. J.E.; Hyros, N.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A;Title: A single rat fibronectin gene generates three different mRNAs by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibronectin precursor - rat
C;Species: Rattus norvegiue (Norway rat)
C;Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text change 09-Jul-2004
C;Accession: S14428; S12455; Ā22319; S46203; S00459; A27252; IS9049
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Matches:
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A;Status: nucleic acid sequence not shown
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A;Accession: S14428
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Best Local Similarity:
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                                                                                                                                                                                                        C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26452; B21165; Ā23292
R;Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.
Bur. J. Biochem. 161, 441-453, 1986
A;Title: Complete primary structure of bovine plasma fibronectin.
A;Reference number: A26452; MUID:87054047; PMID:3780752
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fibronectin - bovine
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1400

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1520

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1580

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1460

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F;1992-2074/Domain: fibronectin type III repeat homology <FN3P>
F;2181-2183/Region: cell attachment (R-G-D) motif
F;2181-2273/Domain: fibronectin type III repeat homology <FN3Q>
F;2295-2335/Domain: fibronectin type I repeat homology <IF10>
F;2381-2378/Domain: fibronectin type I repeat homology <IF10>
F;2381-2378/Domain: fibronectin type I repeat homology <IF11>
F;2381-2420/Domain: fibronectin type I repeat homology <IF12>
F;2381-2378,2385-2411,2409-2420/Disulfide bomds: #status predicted
F;2458/Disulfide bonds: interchain (to 2452) #status predicted
F;2458/Disulfide bonds: interchain (to 2458) #status predicted
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C;Species: Streptococcus pyogenes
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S7680
C;Accession: S77680
B;Kapur, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser Mol. Microbiol. 16, 509-519, 1995
A;Title: Molecular population genetic analysis of the streptokinase gene of Streptococci A;Refactue: Lanslation not shown
A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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A;Cross-references: UNIPROT:Q54687; UN
A;Experimental source: strain ET51/M17
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C,Superfamily: streptokinase
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A,Reference number: A22319; MUID:84298097; PMID:6089177
A,Accession: A22319
A,Molecule type: DNA
A,Recsaidues: 2052-2237 <-TAM>
A,Cross-references: UNIPARC:UPIO000177AEB
A,Residues: 2052-2237 <-TAM>
A,Cross-references: UNIPARC:UPIO000177AEB
R,Falkenberg, C.; Enghild, J.J.; Thogersen, I.B.; Salvesen, G.; Akerstroem, B.
Biochem. J. 301, 745-751, 1994
A,Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in A,Reference number: S46203
A,Accession: 846203
A,Accession: S46203
A,Accession: G46203
A,Accession: G46203
A,Accession: S6203
A,Accession: S620459
A,Accession: S620459
A,Accession: S6459
A,Accession: S6459
A,Accession: S6459
A,Accession: S6459
A,Accession: S6459
A,Accession: MUID:88654950; PMID:3119323
A,Accession: S6459
A,Accession: A,Acce
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A.Residues: 1586-1720, T',1722,1813-2477 <SC2>
A.Cross-references UNIPARC:UPION00177AF0
A.Cross-references UNIPARC:UPION00177AF0
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A.Title: Repeating modular structure of the fibronectin gene: Relationship to protein st
A.Reference number: IS9049; MUID:86016741; PMID:3863113
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A;Molecule type: DNA
A;Residues: 1722-1810 <RES>
A;Cross-references: UNIPARC:UP1000000040C; GB:M11750; NID:g204164; PIDN:AAA41170.1; PID:
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streptokinase A (EC 3.4...) (allele 10) - Streptococcus pyogenes (fragment)
C;Species: Streptococcus pyogenes
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: 877679
R;Kapur, V,; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser
Mol. Microbiol. 16, 509-519, 1995
A;Title: Molecular population genetic analysis of the streptokinase gene of Streptococc
A;Accession: 877679
A;Reference number: 877671; MUID:96037795; PMID:7565111
A;Accession: 877679
A;Accession: 877679
A;Residues: Lranslation not shown
A;Molecule type: DNA
A;Residues: 1-128 cKAP>
A;Residues: 1-128 cKAP>
A;Residues: 1-128 cKAP>
A;Cross-references: UNIPROY:054686; UNIPARC:UP1000008806F; EMBL:U25861; NID:9818924; PI
A;Experimental source: strain ETSO/M43
C;Genetics:
C;Superfamily: streptokinase
C;Superfamily: streptokinase
C;Keywords: hydrolase; plasminogen activator; virulence
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       GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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S7768
streptokinase A (EC 3.4...) (allele 19) - Streptococcus pyogenes (fragment)
C;Species: Streptococcus pyogenes
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: 877688
R;Kapur, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser, Mol. Microbiol. 16, 509-519, 1995
A;Title: Molecular population genetic analysis of the streptokinase gene of Streptococcu A;Scession: 877688
A;Reference number: 877688
A;Reference number: 877671; MUID:96037795; PMID:7565111
A;Residues: L-128 «KAP>
A;Residues: 1-128 «KAP>
A;Cross-references: UNIPROT:Q56695; UNIPARC:UPI00000BDBDC; EMBL:U25870; NID:g818942; PIC
C;Genetics:
A;Gene: ska
C;Superfamily: streptokinase
C;Keywords: hydrolase; plasminogen activator; virulence
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US-09-940-235-10 (1-1661) x S77680 (1-128)
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93 LysProGluSerGluGluThrCysPheAspLysTyrThrGlyValSerTyrArgValGly 112
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Job time : 40.4546 secs
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121 LysGluLysThrAsnAsnThrAsp 128
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US-09-940-235-10 (1-1661) x A43908 (1-2481)

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15 LeuServalvalLeuArgAlaAlaProSerAlaThrSerLysLysArgArgGlnAlaGln

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED GREETION - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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"Complete amino acid sequence of streptokinase and its homology with
"Complete amino acid sequence of streptokinase and its homology with
serine proteases.";
Blochemistry 21:6520-6625(1982).
-!- FUNCTION: This protein is not a protease, but it activates
plasminogen by complexing with it. As a potential virulence
factor, it is thought to prevent the formation of effective fibrin
barriers around the site of infection, thereby contributing to the
invasiveness of the cells.
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01-APR-1988 (Rel. 07, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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MEDLINE=83127125; PubMed=6760891;
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                                            Streptococcus.
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-Q=/Cgn2_1/USPTO_bpool_p/USO9940235/runat_27012006_144218_27563/app_query.fasta_1.7708
-Q=/Cgn2_1/USPTO_bpool_p/USO9940235/runat_27012006_1.1-LOOPELar-1-LOOPERAT=0
-UNITYS=bits -CTART=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=15 - MODE-LOCAL
-USRPACE-USO9940235_@CGN 1 1 1359 @runat_27012006 144218_27563 - NCPU=6 - ICPU=3
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(c) 1993 - 2006 Compugen Ltd.
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     ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
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OS Streptococcus equisimilis.
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EMBL; K02986; AAA26974.1; -; Genomic_DNA.

R PIR; AA2801; CAA51351.1; -; Genomic_DNA.

R PIR; AA2801; BZSO.

R PDB; 1BML; X-ray; BZSO.

R PDB; 1LMD; X-ray; B=40-173.

R PDB; 1LMZ; X-ray; B=40-173.

R PDB; 1LMZ; X-ray; B=27-173.

R PDB; 1LMZ; X-ray; B=27-173.

R R PDB; 1CQC; X-ray; B=30-8.

R R PDB; 1CQC; X-ray; B=27-173.

R PDB; 1CQC; X-ray; B=40-177-314.

R R InterPro; IRR040031, Staphylokinase.

R InterPro; IRR04003124; Streptokinase.

R PEam; PPO2821; Staphylokinase.

R PRINTS; PRO1753; STREPKINASE.

R AB-1 STREPKINASE.

R 3D-structure; Direct protein sequencing; Plasminogen activation; Signal, Virulence.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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P NUCLEOTIDE SEQUENCE.

A Estrada M.P., Hernandez L., Perez A., Rodriguez P., Serrano R.,

Bubiera R., Pedraza A., Padron G., Antuch W., la Fuente J., et al.;

"High level expression of streptokinase in Escherichia coli.";

I Biotechnology 0:1138-1142(1992).

E RMB., 246536, AAC60418.1; -; Genomic_DNA.

PDB., 1C4P; X-ray; A/B/C/D=149-285.

RMS, 053284; 12-372.

RGO; GO:0005515; F:protein binding; IEA.

GO; GO:0005515; F:protein binding; IEA.

InterPro; IPR004093; Staphylokinase.

InterPro; IPR008124; Streptokinase.

R Ffam; PP02821; Staphylokinase;

R Ffam; PP02821; Staphylokinase;

R Ffam; PP02821; Staphylokinase;
                                          al.;
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SEQUENCE 414 AA; 47254 MW; P75BE5831B766904 CRC64;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE-89160265; PubMed-2922269;
Walter F., Siegel M., Malke H.;
"Nucleotide sequence of the streptokinase gene from a
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5521F8825FE1B6EA CRC64;
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Matches:
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Indels:
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01-JUL-1989 (Rel. 11, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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Name=skg;
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Raila A., Bessen D.E.;

"Natural selection and evolution of streptococcal virulence genes
"natural selection and evolution of streptococcal virulence genes
"novelved in tissue-specific adaptations.";
J. Bacteriol. 166:110-121 (2004).

R EMBL; AY234137; AAP39957.1; -; Genomic_DNA.

HSSP; O53284; I(47P.

RM; O7X0Y1; 63-398.

GO; GO:01008243; P:plaminogen activity; IEA.

GO; GO:0005515; P:protein binding; IEA.

InterPro; IPR004093; Staphylokinase.

R InterPro; IPR004134; Streptokinase.

R PRINTS; PR01753; STREPKINASE.
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                                             Streptococcaceae;
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                                                                                     STRAIN=D488;
PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;
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Matches:
Conservative:
Mismatches:
Indels:
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                                   Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales;
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1814.00
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                                                                              NUCLEOTIDE SEQUENCE
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Query Match:
DB:
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NCBI_TaxID=1314;
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Indels:
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     InterPro; IPR004093; Staphylokinase
                    InterPro; IPR008124; Streptokinase.
Pfam; PP02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
                                                                                      SEQUENCE 440 AA; 49885 MW;
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STRAIN=88-019;
STRAIN=88-019;
X PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;
X Ralia A., Bessen D.E.;
"Natural selection and evolution of streptococcal virulence genes involved in tissue-specific adaptations.";
T D. Bacteriol. 186:110-121(2004).
R MBL; AX234129; AAP39949.1; -; Genomic_DNA.
R SMR; QXX0X8; 63-298
R GO: GO:0016301; F:kinase activity; IEA.
GO: GO:0008243; F:plasminogen activator activity; IEA.
R GO: GO:0008243; F:protein binding; IEA.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
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STEPPCOKINASE.
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                                                                                                                                                                                                                     STRAIN-SSI-1 (Servitype M3; MEDLINE-SI-1) (Servitype M3; MEDLINE-SI-1) (Servitype M3; MEDLINE-22683278; PubMed=12799345; DOI=10.1101/gr.1096703; Nakagawa I., Kurokawa K., Yamazaki A., Nakata M., Tomiyasu Y., Okahashi M., Kawabata S., Yamazaki K., Shiba T., Yasunaga T., Hayashi H., Hattori M., Hamada S.; Shiba T., Yasunaga T., Hayashi H., Hattori M., Hamada S.; Serptococcus pyogenes reveals a "Genome sequence of an M3 strain of Streptococcus pyogenes reveals into phage evolution."; Carrangement in invasive strains and new insights into phage evolution."; EMBL; AR0814169; AAM80305.1; -; Genomic_DNA.

EMBL; BA000034; BAC64795.1; -; Genomic_DNA.

HSSP; P00779; 114D.
                                                                                                                        GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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                              L.D.,
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STRAIN-MGAS115 / Serotype M3;
MEDLINE-22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
MEDLINE-22133808; PubMed=1212206; DOI=10.1073/pnas.152298499;
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.; Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O1-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Streptokinase A.
Name=ska; OrderedLocusNames=SPs1700, SpyM3_1698;
Streptococcus pyogenes (serotype M3).
Streptococcus; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
CNEL_TaxID=301448;
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GO; GO:0008243; F:plasminogen activator activity; IEA.
GO; GO:0005515; F:protein binding; IEA.
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Pfam; PF02821; Staphylokinase.
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SEQUENCE 440 AA: 49911
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Q8K5R8; Q79W73;
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STRAIN=SFST70 ( ATCC 700294 ( Serctype M1, STRAIN=SFST70 ( ATCC 700294 ( Serctype M1, STRAIN=SFST70 ( ATCC 700294 ( Serctype M1, Serich D.J., Bavic D.J., Bavic D.J., Bavic D.J., Bavic D.J., Bavic D.J., Bavic D.J., Savic G., Lyon K., Primeaux C., Seate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., A Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E., "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

T. Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

C. -! FUNCTION: This protein is not a protease, but it activates plasminogen by complexing with it. As a potential virulence factor, it is thought to prevent the formation of effective fibrin barriers around the site of infection, thereby contributing to the invasiveness of the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                        GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1262
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AspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsn 346
                                                                                    TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTACAACAATCTC
                                   from a Streptococcus
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                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=SF130/13 / Serotype M1;
MEDLINE=89160264; PubMed=2646590;
Walter F., Siegel M., Malke H.;
"Nucleotide sequence of the streptokinase gene
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EMBL; AE006620; AAK34665.1; -; Genomic_DNA.
PIR; S02724; S02724.
HSSP; Q53284; 1C4P.
SMR; P10520; 63-399.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR00414; Streptokinase.
Pfam; PF02811; Staphylokinase.
PRINTS; PR01753; STREPKINASE.
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16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation updat
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Nucleic Acids Res. 17:1261-1261(1989).
                                                                                                                                                                                                                                                                                                                       Name=ska; OrderedLocusNames=SPy1979
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AC Q7X0Y2;
DT 01-OCT-2003 (TEEMBLrel. 25,
DT 01-OCT-2003 (TEEMBLrel. 25,
DT 01-MAR-2004 (TEEMBLrel. 25,
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|IleAlaGlyTyrGlyTrpLeuProAspArgProProIleAsnAsnSerGlnLeuValVal
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STRAIN=86-779;
PubMed=1467951;
Stalia A., Besen D.E.;
"Natural selection and evolution of streptococcal virulence genes involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).
SEMBL, AX234128; AAP39948.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                    13.5EP-2005 (TrEMBLrel. 31, Created)
13.5EP-2005 (TrEMBLrel. 31, Last sequence update)
13.5EP-2005 (TrEMBLrel. 31, Last annotation update)
13.5EP-2005 (TrEMBLrel. 31, Last annotation update)
Streptokinase.
Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
NCBI TaxID=1314;
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Q532X6 STRPY PRELIMINARY;
Q532X6;
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Best Local Similarity:
Query Match:
DB:
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0008243; F:ptasminogen activator activity; IEA.

GO; GO:0005515; F:ptotein binding; IEA.

InterPro; IPR004093; Staphylokinase.

InterPro; IPR008124; Streptokinase.
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PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;
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EMBL; AY234130; AAP39950.1; -; Genomic_DNA.
HSSP; Q53284; 1C4P.
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Q7x0Y7;
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                                                                                                                                                                  STRAIN=D306;
PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;
Ralia A., Bessen D.E.;
"Natural selection and evolution of streptococcal virulence involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).
EMBL; AY234136; AAP39956.1; -; Genomic_DNA.
SMR; Q7X0Y2; 63-398.
                                         Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator activity; IEA.
GO; GO:0005515; F:protecin binding; IEA.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR008124; Streptokinase.
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Matches:
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1787.00
94.26%
89.30%
60.80%
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                                                                                                       NCBI_TaxID=1314;
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                                                                                   Streptococcus.
Streptokinase.
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TRAIN-MGAS1034;

Whomed=15272401; DOI=10.1086/422697;

Rubmed=15272401; DOI=10.1086/422697;

Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.E.,

Banks D.J., Porcella S.F., Martin J.M., Somerville G.A., Musser J.M.;

Woyich J.M., Deleo F.R., Martin of the group A Streptococcus

The regenome complete genome sequence of a macrolide-resistant serotype

T. Infect. Dis. 190:727-738(2004).

BEBL; CP000003; AAT87827.1; -; Genomic_DNA.

SMR; OSX9T6; 63-398.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:plasminogen activator activity; IEA.

GO; GO:0005515; F:plasminogen activator activity; IEA.

RIHEPPO; IPR004093; Staphylokinase.

RIHEPPO; IPR004093; Staphylokinase.

RIHEPPO; IPR00414; Streptokinase.
                                                                                                          GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1262
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                       TIAGACITCAGAGAITTATACGAICCTCGTGAIAAGGCTAAACIACICTACAAQAAICTC
                                                                                                                                                  GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleAsnTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes (serotype M6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Streptochinase (EC 3.4.-.).
OrderedLocusNames=M6_Spy1692;
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SEQUENCE 440 AA; 50160 MW; 1C5AF(
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PRINTS; PR01753; STREPKINASE.
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1758.00
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O5X9T6_STRP6_PRELIMINARY;
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                                1CSAF07907EC7AC8 CRC64;
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Matches:
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                                                                                                                  Gaps:
Pfam; PF02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
                               50160 MW;
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1758.00
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59.82%
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                                                                                                                                                                                              EXTRAIN-WGASSB212 / Serctype M18;

XX MEDLINE-21927593; PubMed-11917108; DOI=10.1073/pnas.062526099;

XX MEDLINE-21927593; PubMed-11917108; DOI=10.1073/pnas.062526099;

XX Smoot J.C., Barblan K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,

XX Mayor V., Daly J.A., Vasay L.G., Musser J.M.;

XX Papur V., Daly J.A., Vasay L.G., Musser J.M.;

XX Genome sequence and comparative microarray analysis of serctype M18

XX Group A Streptococcus strains associated with acute rheumatic fever

XX Totup A Streptococcus strains associated with acute rheumatic fever

XX Totup A Streptococcus strains associated with acute rheumatic fever

XX Totup A Streptococcus strains associated with acute rheumatic fever

XX Totup A Streptococcus strains associated with acute rheumatic fever

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XX Totup A Streptococcus strains associated with acute rheumatic fever

XX Totup A Streptococcus strains associated with acute rheumatic fever

XX HARD, ASABAS, 1., -, Genomic_DNA.

XX FRES, G33284; 1C4P.

XX G0: G0:0016301; F:Rinase activity; IEA.

XX G0: G0:0016301; F:Plasminogen activator activity; IEA.

XX G0: G0:0008243; F:Plasminogen activator

XX G0: G0:0008243; F:Plasminogen activator

XX G0: G0:0008243; F:Plasminogen activator

XX INTEPPRO; IPR004093; Staphylokinase.

XX INTEPPRO; IPR004124; Streptokinase.
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                                                                                                      Streptokinase.
OrderedLocusNames=spyM18_2042;
Streptococcus pyogenes (Serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Matches:
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PRINTS; PR01753; STREPKINASE.
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SEQUENCE 440 AA; 50382 MW;
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1755.00
93.73%
87.21%
59.71%
                                                                   01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                STRP8 PRELIMINARY;
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NCBI_TaxID=301451;
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843 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 902
PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;
A Kalia A., Bessen D.B.;
"Natural selection and evolution of streptococcal virulence genes involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).

E RMB1, A7234134; AAR39954.1; -; Genomic_DNA.

R RSP; Q53284; 1C4P.
SMR; Q7X0Y3; 63-398.

R GO; GO:0008243; F:plasminogen activator activity; IEA.
GO; GO:0005515; F:protein binding; IEA.
R GO; GO:0005515; F:protein binding; IEA.
R InterPro; IPR004093; Staphylokinase.
R InterPro; IPR00124; Streptokinase.
R PRINTS; PR01753; STREPKINASE.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
NCBI_TaxID=1314;
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1023 GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAAAAGTT 1082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 LysGluLysThrAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysClysGly 306
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                                                                                                                                                                                243 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC 302
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       0 0
       Mismatches:
                                                                           US-09-940-235-10 (1-1661) x Q7X0Y0_STRPY (1-440)
                    Indels:
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     84.86%
58.35%
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|PheThrTyrHisValLysAsnArgGluGlnAlaTyrGlnAsnAspAsnLysThrGlyLeu
GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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Natural a., Bessen D.E.;

ThubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;

Ralia A., Bessen D.E.;

Involved in tissue-specific adaptations.";

Involved in tissue-specific adaptations.";

EMBL; AY234138; AAP39958.1; -; Genomic_DNA.

RSP; Q53284; 1C4P.

R SMR; Q7X0V0; G3-398

GO; GO:0008243; F:kinase activity; IEA.

GO; GO:0008243; F:plasminogen activator activity; IEA.

GO; GO:0008243; F:plasminogen activator activity; IEA.

R GO; GO:0008243; Staphylokinase.

InterPro; IPR0040493; Staphylokinase.

R Pfam; PF02221; Staphylokinase.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Q7X0YO STRPY PRELIMINARY;
Q7X0YO;
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NCBI_TaxID=1314;
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DT OO1-OC
DT OO1-MADE
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SEQ ID NO: Sequence 18 SEQ ID NO:

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A20030 SEQ ID NO:
113118 Sequence 46
A200021 SEQ ID NO:
X13400 Streptococc
E01413 DNA sequence
AX368335 Streptoco
AX175891 Sequence
AX030315 Sequence
AX030316 Sequence
AX030316 Sequence
AX030316 Sequence
Continuation (17 o
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AY234130 Streptoco
AY234137 Streptoco
Continuation (17 o
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AX030317 Sequence
AR175894 Sequence
AX030318 Sequence
AY234136 Streptoco
AY234128 Streptoco
CQ872087 Sequence
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         A20009
I13197
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Bacterial fibrin-dependent plasminogen activator
Patent: US 6210667-A 1 03-APR-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  DNA
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99.4%; Pred. No. 0;
ive 0; Mismatches
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/wol_type="unassigned DNA"
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1 from patent US 6210667.
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BA000034 17
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AR143998.1 GI:15105865
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KEYWORDS
SOURCE
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JOURNAL
FEATURES
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A72832 S.equisimil
AR144000 Sequence
B00522 DNA fragmen
105204 Sequence 5
AR068768 Sequence
A20027 SEQ ID NO:
113315 Sequence 42
S46536 SAC-2=strep
CQ797820 Sequence
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A20016 SEQ ID NO:
113204 Sequence 27
113209 Sequence 34
A20015 SEQ ID NO:
                                                             ; Search time 9059.25 Seconds (without alignments) 11181.386 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                5883141 segs, 28421725653 residues
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                                           nucleic search, using sw model
                                                              January 31, 2006, 10:53:18
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Draft entry and hard copy of sequence for [1] kindly provided by J.J.Ferretti, 03-58P-1985.
J.J.Ferretti, 03-58P-1985.
The -35 and -10 regions are located at positions 760-765 and 781-786 respectively and an SD sequence at 808-813. Downstream from the coding region inverted repeats (positions 2176-2190 and 2203-2217) are thought to function as transcription terminators. The nucleotide sequence of sec does not support the hypothesis that the gene has evolved by duplication and fusion, as suggested by internal two-fold AA homologies of its product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKNYLSPGMFALLPALTFGTVNSVQAIAGPEWILDRPSVNNSQL
VVSVAGYVEGTRYQDISLKFPEIDLTSRPAGGSTREQGISPKSKFRPATDGGAMSHKLEK
ADLIKALOGOLIAMYHSNDDYFEPIDLTSRPAGGSTTTTDRNGKVYFRADKOGSYTLPFOPVOE
FILLSGHVRVRPYKEKPIONQAKSVDVEYTVQFTPLNPDDDFRPGLKOTKLLKTLAIGD
TITSQELLAGAQSILAKNHPGYTIYERDSSIVYHDNDIFRILDPMOGFFTYRVKNREQ
AYRINKKSGLNBEINNTDLISEXYYVLKKGRERPYDPPDRSHLKLPTTKYVDVDTNELL
KSEQLLTRASENDLDFFRDIYDPRDKAKLLYNNILDAFGIMDYTLTGKVEDNHDDTNRILL
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Streptococcus dysgalactiae subsp. equisimilis
                                                                                                                                            Streptococcus
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                                     Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
Bacteria, Pirmicutes, Lactobacillales, Streptococcaceae,
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/note="streptokinase signal peptide"
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Mucleotide sequence of the streptokinase
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/protein_id="AAA26974.1"
/db_xref="GI:153809"
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/product="streptokinase"
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/db_xref="taxon:119602"
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/note="prestreptokinase"
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BCT 26-APR-1993

STRSKC 2568 bp DNA linear BCT 26-APR-199 Streptococcus equisimilis (H46A) streptokinase gene, complete cds. K02986

RESULT 2 STRSKC LOCUS DEFINITION ACCESSION

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Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
1 (Dases 1 to 2568)
Ferretti,J.J. and Malke,H.
Streptokinase-coding recombinant vectors
Streptokinase-coding recombinant vectors
THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
Location/Qualifiers
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PAT 15-JUL-1993

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equisimilis

streptokinase. Streptococcus dysgalactiae subsp.

A04926.1 GI:412219 A04926 S.equisimilis skc A04926

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

1015 1075 1135 1195 1255 1315 1016 1375 1076 1435 1136 1495 1196 1555 1256 1615 1376 ö 596 955 929 716 176 836 968 926 equisimilis" CGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGCAAGGCTTAAGTCCAAAATC CATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGA 1317 GAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGG TATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGT TATTGCTGGACCTGACTGCTGCTAGACCGTCCATCTGTCAACAACAACAATTAGTTGT TAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAAT CGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGCAAGGCTTAAGTCCAAAATC **AAAACCATTTGCTACTGATAGTGGGGGGATGTCACATAAACTTGAGAAAGCTGACTTACT** AAAACCATTTGCTACTGATGGGGGGGATGTCACATAAACTTGAGAAAGCTGACTTACT <u> AAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGT</u> CATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGA CAAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACA CAAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACA TGTGCGCGTTAGACCATATAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGT TGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAAACCAAAATCTGTTGATGT GGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAA AGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACT AGCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGA AGCTCAAGCACAAAGCATTTTAAACAAAAACCCCCAGGCTATACGATTTATGAACGTGA CTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTTACCAATGGATCAAGA CTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGA Gaps ; 0 Length 2568, 1. .2568 /organism="Streptococcus dysgalactiae subsp. /mol\_type="unsasigned DNA" /sub\_species="equisimilis" /db\_xref="taxon:119602" Indels 1556 1257 1616 셤 ઠે 셤

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LIALKKORDNAATPMONSKDTIAGFSBAQETWLPVNPNYOEINVADALANODSI FSTYYQ
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complement (1757. 1761)
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complement (2973. .2976)
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complement(136..1749)
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                             pCWP73, pRH10, pWX4"
complement(89. .1761)
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                                                                                               complement (89. .115)
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complement (3244.
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Malke,H., Roe,B. and Ferretti,J.J.
Nucloctide sequence of the streptokinase gene from Streptococcus
equisimilis H46A.
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1,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; re
gene; skc gene; streptokinase; stringent response-like protein.
Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                  CTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTACAACAATCT
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/db_xref="taxon:119602"
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	Qy     1437     TGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAA     1496       Db     5416     TGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAA     5475	OY 1497 CTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCT 1556	QY 1557 CGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGA 1616	OY 1617 CACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAATGCTAGCTA	OY 1677 TCATTTAGCCTATGATAAAGATCGTFATACCGAAGAACGAGAGGTTTACAGCTACCT 1736 	Oy 1737 GCGTTATACAGGGACACCTATACCTGATAACCCTAACGACAAATAA 1782 	T 5 000	LOCUS AR144000 1242 bp DNA linear PAT 08-AUG-2001 DEFINITION Sequence 5 from patent US 6210667. ACCESSION AR144000 VERSION AR144000.1 GI:15105867	ACHWOLDS : ACHWOLD : ORGANISM Unknown: ORGANISM Unknown: Unclassified.	Ree Baci	rce	Cuery Match 69.6%; Score 1240.4; DB 6; Length 1242; Best Local Similarity 99.9%; Pred. No. 2.8e-313; Matches 1241; Conservative 0: Mismatches 1. Indels 0: Gans 0:	CCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT 59	ALGOTTGCTGCTGCTGGGGGGGGGGGGGGGGGGGGGGGGGG	658 GATCTAACATCACGACCTGCTGGAGAAAGACAGAGGCATAAGTCCAAAATCA [	Oy 718 AAACCATTTGCTACTGATGGCGCGATGTCACATAAACTTGAGAAGCTGACTTACTA 777  181 AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA 240  Oy 778 AAGGCTATTGAAGAAATTGATGCGTAACGTCCACAGAAAGCTGACTTTGAGGTC 837

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    Hagenson, M.J. and Stroman, D.W.

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    2568
    /organism="Streptococcus dysgalactiae subsp. equisimilis"
/mol_type="genomic DNA"
    /db_xref="taxon:119602"

                                                                                                                                                         1 (bases 1 to 2568)
1 (bases 1 to 2568)
1 i) (bases 2 to 2568)
1 i) (bases 2 to 2568)
1 ii) (bases 2 to 268)
1 iii) (bases 2 to 2
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819. .896
/product='streptokinase signal peptide'
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CC Strandedness: Single;
CC Strandedness: Single;
CC Copology: Linear;
CC Appotherical: No;
CC **Gource: Strain=Streptococcus equismilis H46A; CC **Gource: Clone;
Ilbrary-streptococcus equismilis H46A; CC **Gource: Clone;
FH Key
FT S'UTR
1. .818
FT S'UTR
1. .818
FT Product='streptokinase signal peptid mat_peptide 897. .2138
FT Product='streptokinase'
FT S'UTR
21.12.13
FT Product='streptokinase'
FT S'UTR
21.12. .2569.
                                                                       Streptococcus dyagalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
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/product='streptokinase'
R 2142. .2569.
Location/Qualifiers
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larity 99.7%; Pred. No. 5.6e-313;
Conservative 0; Mismatches 4;
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(C12N9/70,C12R1:19)
                                                  JP 1985237995-A/1.
                                                                                                                                               Streptococcus.
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Best Local Simi
Matches 1242;
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                                    TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATTCTC
                                              TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGTCAAACTACTCTACAACAATCTC
                                                                                GATGCTTTTGGTATTATGGACTATACCTTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                             GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGATAATCACGATGAC
                                                                                                                              CATITIAGCCTATGATAAAGATCGTTATACCGAAGAAGAACGAGGAAGTTTACAGCTACCTG
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                                                                                                                                                                                                                                                                                                         DNA
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Patent: US 5854049-A 19 29-DBC-1998;
Location/Qualifiers
1. .2566
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                        2566 bp
US 5854049.
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Sequence 19 from patent
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Matches 1243; Conservative
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69.4%; Score 1237; DB 6;
Best Local Similarity 99.6%; Pred. No. 3.1e-312;
Matches 1240; Conservative 0; Mismatches 5;
Yeast production of streptokinase
Patent: EP 0248227-A1 5 09-DEC-1987;
Location/Qualifiers
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    11. 1401
    /organism="unknown"
    /mol_type="unassigned"

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0; Mismatches 21;
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/ Organism="synthetic construct"
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   PROTEINS AND NUCLEIC ACIDS
Patent: WO 9109125-A 35 27-JU
Location/Qualifiers
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SEQ ID NO: 35; Synthetic nucleotide sequence for Hirudin-streptokinase fusion protein.
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1486 AGCGAACGTAACTTAGAC	1486 AGCGAACGTAACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTC 1545 	<i>&amp;</i> 43	946 CTAAGGGACATGTGGGGTTAGACCATATAAAGAAAACCAATACAAAACCAAGGGAAA 1005 
1546 TACAACAATCTCGATGCT 	TACAACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGAT 1605 	 & 8	1006 TCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGA 1065 
1606 AATCACGATGACACCAAC 	166 133		CCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACTT 11
1666 AATGCTAGCTATCATTA 	aatgctagctatcatttagcctatgataaagatcgttataccgaagaacgagaagtt 1725 	<b>&amp;</b> 8	1126 CAAGAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATT 1185 
1726 TACAGCTACCTGCGTTAT 	TACAGCTACCTGCGTTATACAGGGACACCTATACCTGATAACCCTAACGACAATAA 1782 	& 8 8	1186 TATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCA 1245 
T 10	;	 & 8	1246 ATGGATCAAGAGTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAA 1305 
113215 ON Sequence N 113215 I13215.1	1458 bp DNA linear PAT 26-JUL-1995 42 from patent US 5434073. GI:910563	č a	1306 AAATCTGGTCTGAATGAAGAAATAAACAACTGACCTGATCTCTGAGAAAATATTACGTC 1365 
_		& 8 ————	1366 CTTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACC 1425 
REFERENCE 1 (bases 1 to 1458) AUTHORS Dawson, K., Hunter, M., TITLE Fibrinolytic and ant OURNAL Patent: US 5434073-A	<pre>1 (bases 1 to 1458) Dawson,K., Hunter,M.G. and Czaplewski,L.G. Fibrinolytic and anti-thrombotic cleavable dimers Patent: US 5434073.A 4 2 18-JUL-1995;</pre>	ò a	1426 ATCAAATACGTTGATGTGGGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCT 1485 
ource	l1458 /organism="unknown" /mol_type="unassigned DNA"	& 8	1486 AGCGAACGTAACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTC 1545 
Query Match Query Match Best Local Similarity 98.3%; Matchot 1023	Score 1223.4; DB 6; Length 1458; Pred. No. 1.1e-308;	& 8	1546 TACAACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGAT 1605 
OY 526 ACCGATGTTCGTATTGCT  OY 196 ATCGAGGTTGGATGCTATTGCTATTGCTATTGCTATTGCTATTGCTATTGCTATGAGTTTGCTATGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGGA	8=8	<i>8</i>	1606 AATCACGATGACACACACGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGG 1665 
586 256 256	TTAAA 	& a	1666 AATGCTAGCTATCATTTAGCCTATGATAAGATCGTTATACCGAAGAAGAACGAGAAGTT 1725 
646 316		<i>ò</i> 8	1726 TACAGCTACCTGCGTTATACAGGACACCTATACCTGATAACCCTAACGACAAATAA 1782 
Oy 706 AGTCCAAAATCAAAACCA 	agtccaaaatcaaaaccatttgctactgatagtggggggatgtcacataaacttgagaaa 765 	RESULT 11 S46536 LOCAL	846536 1245 bp DNA lines
766 GCTGACTTACTAAAGGCT 	GCTGACTTACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGAC 825 	ACCESSION VERSION	SNC-2=Bireproximate (Streprococcus equisimitis, group c, Genomic, 1245 nt]. 846536 846536.1 GI:257196
Qy 826 TACTTTGAGGTCATTGAT 	TACTTTGAGGTCATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAAGGCGAAGGTC 885 	SOURCE SOURCE ORGANISM	Streptococcus dysgalactiae subsp. equisimilis Streptococcus dysgalactiae subsp. equisimilis Bacteria, Pirmicutes, Lactobacillales, Streptococcaceae, Streptococcus.

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                                                                                     GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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and ramos gonz Lez,O.
Vector for the production of transplastomic angiosperm plants
Patent: WO 200403925-A 26 08-APR-2004;
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                    /protein_id="AGC60418.1"
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/translation="TAGPBWILDRPSVNNSQLVVSVAGTVEGTNQDISLKFFEIDLTS
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ELLYNNLDAFGIMDYTTTGKVEDNHDDTRNIITVYMGKREGENASYHLAYDKRYK
EREVYSYLRETFIPPDNPNDK"
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/gene="SKC-2"
/note="skreptokinase; Mature protein lacks initial Met"
/codon start=1
/product="SKC-2"
                                                                                                             GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 115306] from the original journal article. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 AGCGTTGCTGGTACTGTTGAGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC
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                     Serrano, R. Fuente, J.
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High level expression of streptokinase in Escherichia coli
Biotechnology (N.Y.) 10 (10), 1138-1142 (1992)
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                     Rodriguez, P.
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Estrada,M.P., Hernandez,L., Perez,A., Rodriguez,P
Rubiera,R., Pedraza,A., Padron,G., Antuch,W., de
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Pred. No. 1.8e-308;
0; Mismatches 14;
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TITSQELLAQAQSILNKTHPGYTIYERDSSIVTHDNDIFRTILPMDQFTYHVKNREQ
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KSEQLLTASERNLDFRENLYDPRAKLLYNNLDAFGIMDYTLTGKVEDNHDDTNRIIT
VYMGKRPEGENASYHLAYDKDRYTEBERBVYSYLRYTGTPIPDNPNDK"
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/organisma="Streptococcus dysgalactiae subsp. equisimilis"
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/sub_species="equisimilis"
/db_xref="taxon:119602"
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 TTAGACTTCAGAGATTTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
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                                   GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                    CATTTAGCCTATGATAAAGATCGTTATACCGAAGAAGAACGAGAAGTTTACAGCTACCTG
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Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Pred. No. 6.8e-308;
0; Mismatches 16;
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Patent: WO 9109125-A 14 27-JUN-1991;
Location/Qualifiers
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gene.
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/db_xref="G1:1247580"
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SEQ ID NO: 14; Streptokinase
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/transl table=11
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Best Local Similarity 98.7
Matches 1230; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1497
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                                                                                                                                                                                                      GATÀCTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
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                                                                                                                                                     ATTGCTGGACCTGATGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTAGTTGTT
                                                                                                                                                                                     AGCGTTGCTGGTACTGTTGAGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATC
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                                                                                                                    ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT
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between the rice atpB and tobacco rbcL borders
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                                           Score 1222.6; DB 6
Pred. No. 1.9e-308;
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LOCUS	Query Match         68.5%;         Score 1220.4;         DB 6;         Length 1335;           Beet Local Similarity         98.7%;         Pred. No. 6.8e-308;           Matches 1230;         Conservative         0;         Mismatches         16;         Indels         0;         Gaps           S37         TATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACACACCCAATTGGTTGT	DD	Qy 657 CGATCTAACATCACGACCTGCTCATGGAGGAAAGACAAGGCTTAAGTCCAAAATC 716	Qy     717 AAAACCATTIGCTACTGATGGGGGGATGTCACATAAACTTGAGAAAGCTGACTTACT 776       Db     264 AAAACCATTIGCTACTGATAGTGGCGCGATGCCACATAAACTTGAAAAGCTGACTTACT 323	Qy 777 AAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTGAGGT 836	Qy 837 CATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGA 896	Qy     897 CAAAGAIGGITCGGIAACCTIGCCGACCCAACCTGICCAAGAAITITIGCIAAGCGGACA     956       Db     444 CAAAGAIGGITCGGIAACCTIGCCGACCCAACCTGICCAAGAAITITIGCIAAGCGGACA     503	Qy 957 TGTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGGAAATCTGTTGATGT 1016	OY 1017 GGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAA 1076	Qy 1077 AGATACTAAGCTATTGAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACT 1136	OY 1137 AGCTCAAGCATTTTAAACAAAACCACCAGGCTATACGATTTATGAACGTGA 1196	Qy     1197 CTCCTCAATCGTCACTCAGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGA 1256       Db     744 CTCCTCAATCGTCACTCATGACATTTTCCGTACGATTTTACCAATGGATCAAGA 803	Qy 1257 GTTTACTTACGGGTTAAAAATGGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCT 1316
	1017 GGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAA	DD 624 AGAIACIAAGCIAITGAAAACACIAICGGIGACACCATCACATCA	Oy         1197         CTCCTGAATGGCACTCATGACATTTCCGTACGATTTTACCAATGGATCAAGA         1256           Db         744         CTCCTCAATGGTCACTGATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGA         803	OY 1257 GITTACCGIGITAAAAAICGGGAACAAGCITATAGGAICAATAAAAATCIGGIC 1316 	OY 1317 GAATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGG 1376 	OY 1377 GGAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGT 1436 	OY 1437 TGATGTCGATACCAACTAGTGAAAGTGAGCGGCTCTTAACAGCTAGCGAAGGTAA 1496 	OY 1497 CTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCT 1556	Oy 1557 CGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGA 1616 	OY 1617 CACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAATGCTAGCTA	OY 1677 TCATTTAGCCTATGATAAGATCGTTATACCGAAGAAGAACGAGAAGTTTACAGCTACCT 1736 	OY 1737 GCGTTATACAGGGACACCTATACCTGATAACCCTAACGACAAATAA 1782 	RESULT 14

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AACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAAT 1608
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                                                                                                                                                                 CCAAAATCAAAACCATTTGCTACTGATAGTGGGCGCGATGCCACATAAACTTGAAAAAGCT
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                                                                                                    GATAAAAGAATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAA
                                                                                                                                         TIGGITGITAGCGITGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTT
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                                                              GATGTTCGTATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTC
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                        21;
    Pred. No. 6.8e-308
0; Mismatches 21
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BGDFDVAVLPFSNSTNNGLLFINTTASIAAKEBGVSLDKRIAGFBWLLDRPSVNNSQ
LVVSVAGTVEGTNDDISLKFPEIDLTSRPAHGGKTROGALDFKSKPPATDSGAMPHKLE
KADLLKAIQRQLIANVHSNDDYFBAUDGPASDATITDRNGKVYFADKOGSYTLPTQPVO
BFLLSGHVRVRPYKBKPIONQAKSVDVEYTVQFTPLNPDDDFRPGLKOTKLLKTLATQ
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LKSBQLLTAASERNLDFRDKAKLLYNNLDAFGINDYTLTGKVEDNHDDTNRII
TVYMGKRPEGGNASYHLAYDKDRYTEEERREVYSYLRYTGTPIPDNPDK"
                                          1376
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streptokinase fused to yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTAGACTTCAGAGATTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCT
  GTTTACTTACCATGTCAAAAATCGGGAACAAGCTTATGAGATCAATAAAAAATCTGGTCT
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                                                                                                                                                                                               TGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAA
                                                                                                                                                                                                                                     984 TGATGTCAACACCAACGAATTGCTAAAAAGCGAGCAGCTCTTAACAGCTAGCGAACGTAA
                                                                                                                                           924 GGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAATACGT
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/mol_bref="taxon:32630"
/u.1506
/codon_start=1
/transl_table=11
/transl_table=11
/product="streptokinase fused to }
/db_xref="GI:1247851"
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Patent: WO 9109125-A 24 27-JUN-1991;
Location/Qualifiers
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synthetic construct
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1068

792

732

1128

852

1188

912

1248

972

1308 1032 1368 1092 1428 1488 1212

Match

Query

ORIGIN

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1273 AACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAAGATAAT 1332
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Search completed: February 1, 2006, 04:17:48 Job time: 9060.25 secs

Aaq12490 Factor Xa
Aaq05603 Streptoki
Aan01016 DNA encod
Aan50493 Sequence
Aat29961 Vector ps
Aaf8114 Mutant st
Aaz99250 DNA encod
Aaa7647 Chimeric
Aaa37644 Chimeric
Aaa37644 Chimeric
Aaa37644 Chimeric
Aaa37645 Chimeric
Aaa37645 Chimeric
Aaa37645 Chimeric
Aaa37645 Chimeric
Aaa17641 Met-core
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Aaq12163 Streptoki
Abn70192 Streptoki
Abn70192 Streptoki
Abn70192 Streptoki
Abax83589 Recombina

Aaq10230 Syntheric Aax80494 Recombina Aad09265 pr7-TACS Ad817488 Nucleotid Adr97657 Human fib Adw44479 Human fib

RESULT 1

Database :

Adf48644 Streptoco

3

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ADR97657
ADW44479
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AAZ92250
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                    13
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11212.4
11212.4
11201.8
1199.6
1189.6
1181.4
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1093.6
1093.6
1093.6
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984.6
January 31, 2006, 10:44:08; Search time 1077.25 Seconds (without alignments) 11024.772 Million cell updates/sec
                                                                                   1 tegetteaegttegetegeg.......ataaeeetaaegaeaaataa 1782
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      GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                     4996997 segs, 3332346308 residues
                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1782
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Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:\* geneseqn2004as:\* geneseqn2004bs:\* geneseqn2005s:\*

Description		Aaa37643 Chimeric Aax80497 Streptoki		Aaa37633 S. equisi	Aag11651 FB-FB-SK	Aax80492 Streptoco	Aba05546 Streptoki	Aba05547 Maxadilan	Aax16632 Streptoco	Aax16633 Streptoco	Aaa37628 Streptoki	Aat77778 Coding se	Aaq12162 Factor Xa	Adm01294 Plasmid p	Aaq12156 Streptoki	Aaq12158 Streptoki		
SUMMARIES	AAA37642	AAX37643 AAX80497	AAA37622	AAA37633	AAQ11651	AAX80492	ABA05546	ABA05547	AAX16632	AAX16633	AAA37628	AAT77778	AAQ12162	ADM01294	AAQ12156	AAQ12158	AAQ12160	AAQ20665
DB	m (	m N	ო	٣	~	~1	9	9	~	~	m	7	~	12	~	7	~	7
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& Query Match	100.0	94.5 69.9	6.69	69.8	69.7	9.69	9.69	9.69	69.5	69.3	69.1	69.0	68.7	9.89	68.5	68.5	68.5	68.4
Score	1782	1684	1245	1243.4	1241.8	1240.4	1240.4	1240.4	1238.8	1235.6	1232.2	1230.4	1223.4	1222.6	1220.4	1220.4	1220.2	1219.4
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AAA3	AAA37642 ID AAA37642 standard; DNA; 1782 BP. ***
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ž	1750 CWW
DŢ	15-SEP-2003 (revised)
Į	13-OCT-2000 (first entry)
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DE	Chimeric SK-FBD coding sequence.
ž	
K	Streptokinase; SK; hybrid plasminogen activator; fibrin binding region;
¥	plasminogen; human; fibronectin; thrombolytic therapy;
₹.	cardiovascular disorder; ss.
ž	
S	Streptococcus dysgalactiae subsp. equisimilis.
SO	Homo sapiens.
SO	Chimeric.
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M	EP1024192-A2.
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PD	02-AUG-2000.
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PF	23-DEC-1999; 99EP-00310541.
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Æ	24-DEC-1998; 98IN-DE003825.
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L I	Sahni G, Kumar R, Roy C, Rajogopal K, Nihalani D, Sundaram V;
PI	Yadav M;
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S S	WPI; 2000-516032/47.
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ᇤ	ding domain poly
1 E	chromotyric instanty comprises a streptokinase tused with libilin binding
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This sequence represents a chimeric streptkinase-fibrin binding domain (SK-PBD) protein coding sequence. The invention relates to a hybrid

Example 5; Fig 21b; 58pp; English.

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Firefactories (SK), which are capable of plasminogen (PG) activation, and fibrin binding regions of human fibronectin, which are from fibrin binding regions of human fibronectin, which are from fibrin binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain colypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating plasminogen activation encountered during clinical use overcomes systemic plasminogen to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2001 to standardise OS field) plasminogen activator (PA) \$

g g g g g g g ઠે 셤 ò Š 8 8 8 셤 ò ò 엄 ò ઠ g δ 8 g ઠે 셤 8 요 ò g d ઠ ò 120 120 180 180 240 240 300 300 360 360 420 420 480 480 540 540 600 9 99 099 720 9 TCGCTTCACGTTCGCTCGCGTATCGGTGATTCATTCTGCTAACCAGTAAGGCAACCCCGC CAGCCTAGCCGGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGGCCAGGACCCA GCTGGACCTGACTGCTAGACCGTCCATCTGTCAACAACAACAATTGGTTGTTAGC CTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCAAAA TCGCTTCACGTTCGCTCGCGTATCGGTGATTCATTCTGCTAACCAGTAAGGCAACCCGGC ACGCTGCCCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCACAAC ACGCTGCCCGAGATCTCCGCCGAAATTAATACGACTCACTATAGGGAGACCACAAC GGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGTGCAAGC GGTTTCCCTCTAGAAATAATTTTGTTTAACTTTTAAGAAGGAGATATACCATGGTGCAAGC ACAACAGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGT CTAGAAATAGATGC GGTCGGAGAAACGTGGGAGAAGCAGCGACGCATCACTTGCACTTCTAGAAATAGATGC AACGATCAGGACACAAGGACATCCTATAGAATTGGAGGACACCTGGAGCAAGGATAAT CGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACCGGCGAGGAGGTGGAAGTGTGAG AGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTATT GTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATCGAT GTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATCGAT AACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAAT GCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTTAGC ö DB 3; Length 1782; Sequence 1782 BP; 573 A; 407 C; 377 G; 425 T; 0 U; 0 Other; Indels GGTCGGAGAAACGTGGGAGAAGGCAGCGGACGCATCACTTGCACTT ö 0; Mismatches 100.0%; Score 1782; 100.0%; Pred. No. 0; Conservative Best Local Similarity Matches 1782; Conserv н 61 121 Query Match 121 241 61 181 361 601 199 181 301 301 361 421 421 481 481 541 501 8 6 B 6 셤

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1140 1080 1080 1200 1320 960 960 900 900 GAAGAAATAAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAAGGGGAA CTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCAAAA CCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTAAAG CCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTAAGA GCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACTTTGAGGTCATT GCTATTCAAGAACAATTGATCGCTAACGTCCACAGAAGAACGACGACTACTTTGAGGTCATT GATTTTGCAAGCGATGCAACCATTACTGAAACGGCAAGGTCTACTTTGCTGACAAA GATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAAAA GATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACATGTG GATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACATGTG CGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTGGAA TATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAAGAT TATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAAGAT ACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTAGCT CAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGACTCC CAAGCACAAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGACTCC TCAATCGTCACTCATGACAATGACATTTTTCCGTACGATTTTACCAATGGATCAAGAGTTT TCAATCGTCACTCATGACAATGACATTTTTCCGTACGATTTTTACCAATGGATCAAGAGTTT ACTIACCGIGITAAAAATCGGGAACAAGCITATAGGATCAATAAAAAATCIGGICIGAAT ACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTGAAT GAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGGGAA AAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTTGAT GTCGATACCAACGAATTGCTAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAACTTA GTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAACTTA GACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGAT GACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGAT GCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGACACC GCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGACACC TTAGCCTATGATAAGATCGTTATACCGAAGAAGAACGAGAAGTTTACAGCTACCTGCGT TTAGCCTATGATAAAGATCGTTATACCGAAGAAGAACGAGAAGTTTACAGCTACCTGCGT 1021 1081 1141 1141 1201 1201 1321 1381 1381 1441 1561 1621 1621 1681 1741 1741 721 781 841 841 901 196 1021 1081 1441 1501 1681 721 781 901 961 1261 1261 1321 1501 1561 쉽 Š

51 TCGCTTCACGTTCGCTCGCGTATCGGTGATTCATTCTGCTAACCAGTAAGGCAACCCCGC

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This sequence represents a chimeric streptkinase-fibrin binding domain (SK-FBD) protein coding sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide thision between streptokinase (SK), which are capable of plasminogen (PG) activation, and fibrin binding regions of human fibronectin, which are from fibrin contains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrids have enhanced fibrin selectivity as cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag capaminus in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vacular system without significantly activating the circulating the catalysis of the vascular system without significantly activating the circulating characterial and the natural activation the catalysis of the vascular system without significantly activating the circulating the circulating the circulating the circulating than the matural than the matural than the matural activation of the vascular system without significantly activating the circulating than the matural than the matural than the matural activation of the vascular system without significantly with the paracterial activation of the paracterial activation of the vascular system without significants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
                                                                                                                                                                                                                                                             Streptokinase; SK; hybrid plasminogen activator; fibrin binding region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sundaram
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99.7%; Pred. No. 0;
tive 0; Mismatches 5; Indels 0
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                                                                                                                                                                                                                                                                                     plasminogen; human; fibronectin; thrombolytic therapy; cardiovascular disorder; 88.
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                                                                                                                                                                                                                                                                                                                                                       Streptococcus dysgalactiae subsp. equisimilis
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                                                                                                                                                                                                           Chimeric SK-FBD coding sequence.
                                         AAA37643 standard; DNA; 2096 BP
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1 TGGTTCACGTTCGCTCGCGTATCGGTCATTCTGCTAACCAGTAAGGCAACCCCGC

Best Local Similarity 99.7 Matches 1687; Conservative

N-terminally deleted streptokinase.

P-PSDB; AAY24797

73pp; English.

Example, Page 45-48;

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            GAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGGGAA
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The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; composition comprising a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; a daministering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (I) encoding a modified bacterial streptokinase; (3) an composition comprising (I); and (4) a host cell transformed with the the expression vector comprising (I); and (4) a host cell transformed with the the composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving to bacterial fibrin-dependent plasminogen activator is useful for dissolving composition, venous thrombosis pulmonary embolism, cerebral thrombosis, infarction, venous thrombosis pulmonary embolism, cerebral thrombosis, composition of infarction, venous thrombosis pulmonary embolism, cerebral thrombosis, composition of fibrin than in the absence of fibrin. The modified streptokinase can plasminogen is at least 10-fold, preferably 100-fold grader in activates a streptokinase has at least one amino acid substitution that inactivates a cubstrate site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence composition and altose binding protein fusion protein from
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This sequence represents a streptokinase-NTRN (SK-NTRN) gene (where NTRN stands for N-terminally repaired with native sequence). The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, and fibrin binding regions of human fibronectin, which are created the probability to bind with fibrin independently and also constructed the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident constructed animal or human PG. The hybrid streptokinase-fibrin binding constructed animal or human PG. The hybrid streptokinase-fibrin binding constructed animal or human PG. The hybrid streptokinase-fibrin binding constructed as well as kinetics of plasminogen activation that are distribute from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen to plasmin, thus aiding in the localisation of the plasminogen activation encountered during clinical use conservances systemic plasminogen activation encountered during clinical use conservances systemic plasminogen to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use conservances of the proteins conservances systemic plasminogen activation encountered during clinical use conservances.
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GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
           GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
                                       GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
                                                   GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
                                                                             GCTCAAGCACAAAAGCATTTTAAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
                                                                                           GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
                                                                                                                    TCCTCAATCGTCACACTGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
                                                                                                                                                            TITIACTITACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAATCTGGTCTG
                                                                                                                                                                                                  AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAGGG
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                                                                                                                                                                                                                                                                                                    GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
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                                                                                                                                      TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
                                                                                                                                                                             TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG
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This sequence represents the human Streptococcus equisimilus streptokinase coding sequence. The invention relates to a hybrid presents of plasminogen activator (PA) comprises a polypophide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, and streptokinase (SK), which are capable of plasminogen (PG) activation, and considered by prid AP possesses the binding domains (PBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of cardiovascular streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. allayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use considered busing clinical use considered businese. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
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0; Mismatches
/product= "streptokinase"
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Best Local Similarity 99.5
Matches 1244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kumar R,
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241 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC 300

monomer

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Fibrin-binding protein; fibrinolysis; intravascular thrombi; fibrinogen; streptokinase; fusion protein; ss.
                                                                                                                                                                                                                                                                                        injectable fibrinolytic agent - with affinity by linking agent to fibrin binding domain.
                                                                                                                                  /*tag= c
/label= streptokinase
                                                               Location/Qualifiers
                                                                                                        /*tag= b
/label= FB monomer
359. .1601
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                                                                       10. .184
/*tag= a
/label= FB m
   FB-FB-SK fusion construct
                                                                                                85. .358
                                                                                                                                                                                                                              (CREA-) CREATIVE BIOMOLEC
                                              Staphylococcus aureus.
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P-PSDB; AAR11829.
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            ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAAACGGCAAGGTCTACTTTGCTGAC
                                                                    GTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
                                                                                GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTTCAGACCAGGTCTCAAA
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                                   AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
                                              361 AAAGATGGTTCGGTAACCTTGCCGACCCCAACTGTTTTGCTAAGCGGACAT
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                                    The DNA encodes an FB-FB dimer linked to the streptokinase coding sequence. The FB fragment has selective affinity for fibrin, low affinity for fibrinogen, and minimal immunogenicity, imparting thrombus-targetting capability. See also AAQ11649 and AAQ11650
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                                                                                                                                             Sequence 2030 BP; 673 A; 464 C; 406 G; 487 T; 0 U; 0 Other;
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                                                                                                                                                                                      69.7%; Score 1241.8; 99.8%; Pred. No. 0;
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Disclosure; Fig 5; 18pp; English
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AAQ11651 standard; DNA; 2030

(first entry)

08-JUL-1991

SAXAXEX

97US-0069497P. 98WO-US026694

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myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; asterial thrombosis; ss.
 rSK; bacterial; blood clot; thrombotic condition;
                                            Streptococcus dysgalactiae subsp. equisimilis.
                                                                                                                                                                                                                                                          Claim 44; Page 58-60; 73pp; English.
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The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; composition comprising a blood clot in a subject, comprising cadministering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; a concern comprising (1); and (4) a host cell transformed with the expression vector comprising (1); and (4) a host cell transformed with the cheerial fibrin-dependent plasminogen activator is useful for dissolving concernal fibrin-dependent plasminogen activator is useful for dissolving infarction, venous thrombosis pulmonary embolism, cerebral thrombosis, caraft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammanls. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold grader in activates a streptokinase has at least one amino acid substitution that inactivates a cubstratt site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence concerns an encoded plasminogen native streptokinase at least two-fold. The present sequence of fibrin that streptokinase at least two-fold. The present sequence of encodes native streptokinase at least two-fold. The present sequence of encodes native streptokinase (nSK). (Updated on 17-OCT-2003 to ö 180 837 657 120 717 777 240 9 GATCTAACATCACGACCTCCTCATGGAGGAAAGACAGAGCAAAGGCTTAAAGTCCAAAAATCA AAACCATTIGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA 538 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT 1 ATTGCTGGACCTGAGGCTGCTAGACCGTCCATCTGTCAACACAGCCAATTAGTTGTT AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC 61 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGAGAAAGGCTTAAGTCCAAAATCA AAACCATTIGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC Gaps Length 1242; .; 0 Sequence 1242 BP; 424 A; 267 C; 237 G; 314 T; 0 U; 0 Other; 1; Indels DB 2; Score 1240.4; Pred. No. 0; 0; Mismatches Query Match 69.6%; Best Local Similarity 99.9%; Matches 1241; Conservative standardise OS 181 598 658 121 718 778 셤 \$ 셤 Š 셤 δ

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Streptococcus; streptokinase; fibrin-dependent plasminogen activator;

Streptococcus equisimilis native streptokinase encoding cDNA.

(first entry) (revised)

17-OCT-2003 26-AUG-1999

AAX80492;

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AAX80492 standard; cDNA; 1242

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                                                                         vasodilator; thrombolytic; angina; myocardial infarction;
                                                    gene therapy;
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                                               Streptokinase; cerebroprotective; cardiant;
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iive 0; Mismatches
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                                                                                                 gene therapy; maxadilan; ss.
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Streptokinase cDNA
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RESULT 8 ABA05546 (first entry)

26-FEB-2002

vasodilator; thrombolytic; angina; myocardial infarction; stroke; gene therapy; maxadilan; sand fly; plasmid; ds.

Lutzomyia longipalpis. Unidentified.

Synthetic. Chimeric. WO200185100-A2

11-MAY-2000; 2000US-00569920 10-MAY-2001; 2001WO-US015209

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6294

Streptokinase; cerebroprotective; cardiant; gene therapy; fusion;

Maxadilan-streptokinase fusion protein plasmid pTYB3maxstk

BP

DNA; 8893

ABA05547 standard;

ABA05547

26-FEB-2002

ABA05547;

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in which at least one of the amino acids in the ProS8-Ly859-Ser60-Ly861 segment of the corresponding native SK is replaced by another amino acid. The present sequence encodes native SK is replaced by another amino acid. The present sequence encodes native SK. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPlg) to plasmin (HPlm), which is a serine protease able to catalyse the hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolyric symptoms such as acute myocardial infarction. Compared with wild-type SK, the KS9E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    838 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGCCAAGGTCTACTTTGCTGAC 897
    plasma clot, hydrolysis, haemolytic Streptococcus, plasminogen; plasmin, serine protease; fibrin; blood clot, thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC
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                                                                                                             Streptococcus dysgalactiae subsp. equisimilis.
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99.8%; Pred. No. 0;
ive 0; Mismatches
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                                                                    fibrinolysis; resistance;
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Matches 1240; Conservative
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                                                                                   GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
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The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence encodes mutant SK K59E. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPPg) to plasmin (HPlm), which is a serine protease able to catalyse the hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thrombombolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective
                         plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin, serine protease; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction; fibrinolysis; resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is more resistant to degradation by human plasmin and is more ellective both in acting as a fibrolytic agent and in activating human plasminogen
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                    equisimilis H46A; streptokinase; mutant; fibrinolytic;
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Synthetic.
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This sequence represents a streptokinase-NTR (SK-NTR) gene (where NTR stands for N-terminally repaired with native sequence). The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide (fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, and fibrin binding demains (FBD) 4 and 5 or 1 and 2. The hybrid PA comprises the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after expoure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding comin polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrid streptokinase-fibrin binding as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating overcomes systemic plasminogen co the site of pathological thrombus. This overcomes systemic plasminogen co the site of pathological thrombus. This overcomes systemic plasminogen co the site of pathological thrombus. This overcomes systemic plasminogen coultaring on standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
                                                                             Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy;
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99.4%; Pred. No. 0;
ive 0; Mismatches
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                                       Streptokinase-NTR gene
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Yadav M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes the wild type plasminogen-binding fragment of streptokinase. The protein fragment encoded by this sequence was used in the design of a modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, opt. as a bolus rather than by continuous infusion. (Updated on 17-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified forms of streptokinase resistant to enzymatic cleavage - usefi
as thrombolytic agents in treating thrombosis and in medical equipment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                537 TATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGT
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                                                                                                        Coding sequence for plasminogen-binding fragement of Streptokinase.
                                                                                                                                                    dв.
                                                                                                                                    fragment; streptokinase; degradation; MBP;
blood clot; bolus; maltose-binding protein;
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                                                                                                                                                                                   Streptococcus dysgalactiae subsp. equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%; Score 1230.4; 99.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 22-23; 65pp; English.
AAT77778 standard; cDNA; 2566 BP.
                                                                                                                                                                                                                                                                              96WO-US009640
                                                                                                                                                                                                                                                                                                             95US-00488940.
                                                           (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE
                                                                                                                                    Plasminogen-binding
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-065469/06.
                                                                                                                                                        thrombolytic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                              07-JUN-1996;
                                                                                                                                                                                                                                                                                                           09-JUN-1995;
                                                                                                                                                                                                                 WO9641883-A1
                                                         17-0CT-2003
01-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Simi
Matches 1243;
                                                                                                                                                                                                                                                27-DEC-1996
                            AAT77778;
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706 AGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of the synthetic hirudin HV-1 genes was designed based on the published amino acid sequence (Dodt J., et al FEBS Letters 165 180 chromosomal The sequence of streptokinase was obtd. from PCR amplified chromosomal DNA from S. equisimilis ATCC 10009 or ATCC 9642. The primers used for the PCR were based on the pub- lished DNA sequence of S. 497-362 [1985]). The two sequences were used to construct an expression vector in which the hirudin gene is linked to the streptokinase gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also AAQ12153-012156, AAQ12158-Q12161 and AAQ12190. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTTTGAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAAGGCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526 ACCGATGTTCGTATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 ATCGAAGGTAGAATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATTGGTTGTTAGCGTTGCTGCTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 CAATTAGTTGGTTGCTTGCTGTTGTTGAGGGGACGAATCAAGACATTAGTCTTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1458 BP; 491 A; 316 C; 290 G; 361 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Indels
                                                                                                                                                                                                                                           factor Xa cleavage site"
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Pred. No. 0;
0; Mismatches
                                                                                                           /*tag= a
| . . 195
| *tag= b
|/tabel= hirudin HV-1
196. .207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Czapleswsk LG;
                                                                                                                                                                                                                                                                               /*tag= d
/label= streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 96; 115pp; English.
                                                                           Location/Qualifiers
1. .1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BRBI-) BRITISH BIO-TECHNOLOGY LID
                                                                                                                                                                                                         /*tag= c
/label= linker
/note= "encodes f
208. .1449
   antithrombotic; thrombolysis; ss
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90WO-GB001911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dawson KM, Hunter MG,
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07-DEC-1990;
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                          GGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAA
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 CAAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACA
                                                                       TGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGT
                                                                                                1314 TGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAAACCAAAATCTGTTGATGT
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                                                                                                                              TACTITICAGGICATIGATITITICCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGIC
                                                                                                                                                                                     TACTITIGCIGACAAAGAIGGIICGGIAACCIIIGCCGACCCAACCIGICCAAGAAITITITIG
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                                            GCTGACTTACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGAC
                                                                                                  TACTTTGAGGTCATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTC
                                                                                                                                                          TACTTTGCTGACAAAGATGGTTCGCTAACCTTGCCGACCCCAACCTGTCCAAGAATTTTTG
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The invention relates to a DNA vector (A) for stable transformation and expression of genes (I) in plastids, where (I) is inserted in an artificial intergene region (AIR) formed by combining two 5'-untranslated regions (5'-UTRS) of genes that transcribe in different directions and are derived from plants of different divisions or classes. (A) are used to produce transplastomeic anglosperms that have improved agronomic properties (e.g. resistance to biotic or abiotic stress) or express a very wide range of agricultural, veterinary, pharmaceutical, nutritional or industrial products, e.g. enzymes, vaccinating antigens, cytokines or immunoglobulins. Use of (A) eliminates the need for a transposon for gene insertion, inserted genes do not require promoters and terminators, and applicability. Also any selection marker in (A) can be eliminated by chomologous recombination. (A) provides efficient and stable expression of genes without causing any functional alterations. This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA vector for transformation and expression in plastids, useful e.g. for producing pharmaceutical proteins or improving agronomic properties, has gene inserted in artificial intergene region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                            vector; plastid; artificial intergene region; plant;
transplastomic angiosperm; agronomic property; stress resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents the plasmid pVTPA-Estrep, an example of the vector of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 7057;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gonzalez Quintero ADC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7057 BP; 2029 A; 1543 C; 1608 G; 1877 T; 0 U; 0 Other;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Ramos Gonzalez O;
                                                                                                            Plasmid pVTPA-Estrep DNA sequence
ADM01294 standard; DNA; 7057 BP
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98.9%;
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                                                                        (first entry)
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                                                                                                                                                                                                                                                        WO2004029256-A2
                                                                                                                                                                                    rbcL gene; ds
                                                                                                                                                                                                                      Unidentified.
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718 AAACCATTIGCTACTGATAGTGGCGCGGATGTCACATAAACTTGAGAAAGCTGACTTACTA 777

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Job time : 1078.25 secs

	2263 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCAGTAACGACGACTACTTTGAGGTC 2322 838 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAACGGCAAGGTCTACTTTGCTGAC 897	898 AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGGGGACAT 957 	958 GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG 1017 	1018 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 1077 	1078 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 1137 	1138 GCTCAAGCACAAAGCATTTAAACAAAAACCACCAGGCTATACGATTTATGAACGTGAC 1197 	1198 TCTCAATGGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAANGGATCAAGAG 1257 	1258 ITTACTTACCGIGITAAAATCGGGAACAAGCTTATAGGAICAATAAAAATCTGGICIG 1317 	1318 AATGAAGAATAAACAACACTGATCTCTGAGAAATATTACGTCCTTAAAAAGGG 1377 	1378 GARAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 1437 	1438 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1497 	1498 ITAGACTICAGAGAITTATACGAICCTCGIGATAAGGCTAAACTACTCTACAAGAATCTC 1557 	1558 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGATAATCACGATGAC 1617 	1618 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCGAAGGAGAGAATGCTAT 1677 	1678 CATTTAGCCTATGATAAAGATCGTTATACCGAAGAAGAACGAGAAGTTTACAGCTACCTG 1737 	1738 CGTTATACAGGACACCTATACCTGATAACGACAAATAA 1782 

Search completed: January 31, 2006, 18:17:51

Sequence 3, Appli

Sequence 13, Appl Sequence 13, Appl Sequence 1289, Appl Sequence 1, Appli Sequence 13, Appli Sequence 13, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 15, Appl Sequence 11, Appl Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli

Scoring table:

Searched:

Database :

Perfect score:

Sequence:

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OM nucleic

Run on:

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DB 3; Length 2385;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIPICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: ALCOTTORY, Strimpel, Harriet M.
REGISTRATION NUMBER: 1874/111
TELECHONG, (617)443-929
TELEPHONE: (617)443-929
TELEPHONE: (617)443-929
TELEPHONE: (617)443-929
TELEPHONE: 2185 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: TOWNEDDNESS: single
                              US-09-211-542A-13
US-09-220-132-38
US-09-220-132-38
US-09-023-655-1289
US-08-551-356-1
US-09-566-921-135
US-09-813-718-13
US-09-813-718-13
US-09-813-718-15
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US-09-813-718-9
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US-09-813-718-9
US-09-813-718-7
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TOPOLOGY: linear MOLECULE TYPE: cDNA
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LOCATION:
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Query Match
Sequence 1, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 19, Appli
Sequence 42, Appli
Sequence 1, Appli
                                                                        January 31, 2006, 16:24:19; Search time 314.619 Seconds (without alignments) 10068.109 Million cell updates/sec
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Sequence 46,
Sequence 11,
Sequence 11,
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Sequence 34,
Sequence 25,
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. / cgn2_6/ptodata/1/ina/5_COMB.seq:*
. / cgn2_6/ptodata/1/ina/6A_COMB.seq:*
. / cgn2_6/ptodata/1/ina/6B_COMB.seq:*
. / cgn2_6/ptodata/1/ina/H_COMB.seq:*
. / cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
. / cgn2_6/ptodata/1/ina/PP_COMB.seq:*
. / cgn2_6/ptodata/1/ina/PP_COMB.seq:*
. / cgn2_6/ptodata/1/ina/RE_COMB.seq:*
. / cgn2_6/ptodata/1/ina/RE_COMB.seq:*
. / cgn2_6/ptodata/1/ina/RE_COMB.seq:*
         5.1.6
Compugen Ltd.
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US-08-568-3938-2
US-07-854-5968-42
US-07-854-5968-14
US-07-854-5968-14
US-07-854-5968-14
US-07-854-5968-27
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US-09-658-179-13
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S-09-658-179-14
S-07-854-596B-30
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                         1303057 segs, 888780828 residues
        GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     nucleic search, using sw model
                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                      Issued_Patents_NA:*
                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                        US-09-940-235-11
1782
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Match Length
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1245.8 1238.0.4 1238.0.4 1223.0.6 1222.3.0.6 12220.0.4 12220.0.4 1219.0.4 1216.4 11184.4 11184.4

Score

Result

11181.4 11181.4 1093.6 1093.6 1093.6 1093.6 1080.8

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718 AAACCATTIGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA
      1201 GGTTATACAGGGACACCTATACCTGATAACCCTAACGACAAA 1242
                                                                                                                                                                                                                                                                                                        ADDRESSEE: Jeing & Chang
STREET: Two No. 5876999th Second Street, Suite
CITY: San Jose
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB
MEDIUM TYPE: Blokette, 3.50 inch, 1.44MB
MEDIUM TYPE: Storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordDerfect 6.1 on Window 3.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/568,393B
FILING DATE:
CLASSIPTATION WUMBER: 37,798
REFISENTE CHI-PING CHANG
REGISTRATION NUMBER: 37,798
REFISENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 288-8585
TELEPHONE: MANGER TO NUMBER:
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                                                                                                                      Sequence 1, Application US/08568393B; Patent No. 5876999; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (408) 288-8380 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic Acid
STRANDEDNESS: double
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ORGANISM: Streptococcus equisimilis H46A INDIVIDUAL ISOLATE: Malke, H., Roe, B., and Ferretti, J. J.; INDIVIDUAL ISOLATE: "Nucleotide sequence of the streptokinase gene from Streptok INDIVIDUAL ISOLATE: equisimilis H46A CELL TYPE: Streptococcus equisimilis H46A ö 657 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC 120 717 121 GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA 180 777 9 1 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCACCAACAGCCAATTAGTTGTT AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATC GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGGGCAAGGCTTAAGTCCAAAATCA 538 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACACAGCCAATTGGTTGTT Gaps Length 1242; APPLICANT: Hua-Lin Wu
APPLICANT: Hua-Lin Wu
APPLICANT: Guey-Yueh Shi
TITLE OF INVENTION: Preparation of novel streptokinase
TITLE OF INVENTION: mutants as improved thrombolytic agents
TUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 2; Indels

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LOCATION: DNA sequence No. 5876999174 and 175 have been changed LOCATION: from AA to GG, and PROTEIN sequence No. 587699959 has been changed LOCATION: from Lys to Glu.
OTHER INFORMATION:
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Sequence 2, Application US/08568393B
Patent No. 587699
GENERAL INFORMATION:
APPLICANT: Hua-Lin Wu
APPLICANT: Guey-Yueh Shi
TITLE OF INVENTION: mutants as improved thrombolytic agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeing & Chang
STREE: Two No. 5876999th Second Street, Suite 290
CITY: San Jose
STATE: California
COUNTRY: USA
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB
MEDIUM TYPE: Biskette, 3.50 inch, 1.44MB
MEDIUM TYPE: Storage
COMPUTER: STOREM: STOREM: COMPUTER: STOREM: PC-COMPAIDE
COMPUTER: TEM PC COMPAIDE
COMPUTER: WordPerfect 6.1 on Window 3.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,393B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chi.Ping Chang
REGISTRATION NUMBER: 37,798
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69.3%; Score 1235.6;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1238; Conservative 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 288-8585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (408)288-8386
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1242 base pairs TYPE: Nucleic Acid STRANDEDNESS: double
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NAME/KEY: SK-K59E
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ANTI-SENSE: N
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                                                                                                                      ATTGATTTTGCAAGGATGCAACCATTACTGATGGAAACGGCAAGGTCTACTTTGCTGAC
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COMPUTX: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SUGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-JUN-1995
CLASSIFRCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
RECISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELEPHAN: 617/542-5070
TELEFAK: 617/542-5070
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Pred. No. 0;
0; Mismatches
                   Richardson P.C.
                                225 Franklin Street
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SEQUENCE CHARACTERISTICS:
LENGTH: 2566 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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   CORRESPONDENCE ADDRESS
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Best Local Similarity
                                                                            USA
                                               Boston
                                STREET: 2
CITY: BOE
STATE: MA
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 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
                     301 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
                                                               TGCTAAGCGGACAT
                                                                                361 AAAGATGGTTCGGTAACCTTGCCGACCCAACTGTCCAAGAATTTTTGCTAAGCGGACAT
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Patent No. 5854049
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 TTTTTGAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGAAGGCTTA
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fusion linked by Factor Xa cleavable IEGR'
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0; Mismatches
                                                                                                                 92,337
  ETLING LAILS:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUBBER: 26,949
REFERENCE/DOCKET NUMBER: 92,33
TELEPOMMUNICATION INFORMATION:
TELEFAX: 312-715-100
TELEFAX: 312-715-134
TELEX: 910-221-5317
INFORMATION FOR ESG ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 98.3%;
Matches 1236; Conservative 0
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1458
OTHER INFORMATION: /note
OTHER INFORMATION: fusio
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                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid_STRANDEDNESS: single TOPOLOGY: linear
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LOCATION:
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; LOCATION:
US-07-854-5968-42
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                                                                                                                 1317 GAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGG 1376
                                                                                                                                                                                                                                                                                                                                                                                              1674 GAATGAAAAAAAAAAAAAACAACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGG 1733
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AGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACT
                     1434 AGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACT
                                                                                         AGCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGA
                                                                                                                                                                                   CTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGA
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; Patent No. 2434073
; GENERAL INFORMATION:
    APPLICANT: Dawson, Keith M
    APPLICANT: Hunter, Michael G
    APPLICANT: Hunter, Michael G
    APPLICANT: Czaplewski, Lloyd G
    TITLE OF INVENTION: Proteins and nucleic acids
    NURRESPONDENCE ADDRESS:
    ADDRESSEE: Dr. John J. McDonnell
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTE: Floppy disk
COMPUTE: PROPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
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STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
ATATE: IL
COUNTRY: USA
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Properties: Streptokinase gene
The gene product binds to human plasminogen
The gene product is an activator of human plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AAACCATTTGCTACTGATAGTGGCGCGATGCCACATAAACTTGAAAAAGCTGACTTACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            718 AAACCATTIGCTACTGATAGTGGCGCGATGTCACATAAACTTIGAGAAAGCTGACTTACTA
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98.9%; Pred. No. 0;
ive 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus equisimilis from group C organism: Streptococcus equisimilis from group C organism: afforce: ATCC-9542 strain FRATURE: from 1 to 1245 bp mature peptide of FRATURE INFORMATION: Properties: Streptokinase gene OTHER INFORMATION: The gene product binds to human OTHER INFORMATION: The gene product is an activate.
                                                                                                                                                                                                                                                                                           PROTEIN
                  NAME: Michaelson, Peter L.
REGISTRATION NUMBER: 30090
REFERENCE/DOCKET NUMBER: 30090
REFERENCE/DOCKET NUMBER: 30090
TELEPAX: (908) 530-6671
TELEPAX: (908) 530-6671
TELEPAX: (908) 530-6894
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1245 base pairs
TYPE: NUCLEOTIDE WITH CORRESPONDING PRC
STRANDEDNESS: single
TYPE: NUCLEOTIDE WITH CORRESPONDING PRC
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: Genomic DNA
ORIGINAL SOURCE:
ATTORNEY/AGENT INFORMATION:
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Patent No. 5295366

GENERAL INFORMATION:

APPLICANT: Garcia,M.P.E. et al

TITLE OF INVENTION: METHOP FOR THE ISOLATION AND EXPRESSION

TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTORINASE, NUCLEOTIDE SEQUENCE

TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTORINASE, NUCLEOTIDE SEQUENCE

TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTORINASE, NUCLEOTIDE SEQUENCE

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TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTORINASE, NUCLEOTIDE SEQUENCE

TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTORINASE, NUCLEOTIDE SEQUENCE

TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTORINASE, NUCLEOTIDE SEQUENCE

TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTORINASE, NUCLEOTIDE SEQUENCE

TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTORINASE, NUCLEOTION OF A GENE WHICH CODES FOR STREPTORINA OF THE SEQUENCE OF THE STREPTORINA OF THE SEQUENCE OF T
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                                                                           796 CAAGAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAACCCATCCAGGCTATACGATT
                                                                                                                                       TATGAACGTGACTCCTCAATCGTCATCATGACAATGACATTTTCCGTACGATTTTACCA
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OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Microsoft Word for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/703,778D
FILING DATE: 19910522
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2"
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Pred. No. 0;
0; Mismatches 16; Indels
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                                                                                                                                                                                                                                                      /note= "Streptokinase gene from
equisimilis"
TELEX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.5%;
98.7%;
                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: 1..1335
OTHER INFORMATION: /not
OTHER INFORMATION: equi
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Best Local Similarity 98.7
Matches 1230; Conservative
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; NAME/KEY:
; LOCATION:
;
US-07-854-5968-14
                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 1257
                                                                                                                                                                                                                                                                                                                                                                                                             TTAGACTICAGAGATITATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 1557
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                                                                                                                                                                                                                                                                                                                                                    661 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
                                                                                                                  AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG
                                                                                                                                                                                              GABABAGCCGTATGATCCCTTTGATCGCAGTCACTTGABAACTGTTCACCCATCABATACGTT
                                                                                              TITACTTACCGIGITAAAAATCGGGAACAAGCITATAGGATCAATAAAAATCTGGTCTG
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US-07-854-596B-14
US-07-854-596B-14
; Sequence 14, Application US/07854596B
; Patent No. 5434073
; GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
; APPLICANT: Hunter, Michael G
; TITLE OF INVENTION: Proteins and nucleic acids
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UNN-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
STATE: LL
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REGISTRATION INBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606
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                                                                                                                                                                   /note= "Streptokinase
fused to a yeast alpha-factor"
                                                                                                                                                                                                                                                                                                                                                              Query Match 68.5%; Score 1220.4; Best Local Similarity 98.3%; Pred. No. 0; Matches 1233; Conservative 0; Mismatches
           LENGTH: 1512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PRATURE:
                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1..1512
OTHER INFORMATION: /note
OTHER INFORMATION: fused
PEATURE:
NAME/KEY: CDS
LOCATION: 7..1503
FEATURE:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     mat_peptide
7..1503
                                                                                                                                                                                                                                                                                                       ; LOCATION:
US-07-854-596B-27
                                                                                                                                                                                                                                                                                     NAME/KEY:
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                                                                                                            GAATGAAGAAATAAACAACCACTGACCTCATCTCTGAGAAATATTACGTCCTTAAAAAAGG
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                                                                                                                                                                 GGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGT
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIPICATION: 435
ATCORNEY AGENT INPORMATION:
NAME: MCDONNEIL JOHN J
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27,-Application US/07854596B; Sequence 27,-Application US/07854596B; Patent No. 5434073; GENERAL INFORMATION:
APPLICANT: Dawson, Keith M; APPLICANT: Hunter, Michael G; APPLICANT: Hunter, Michael G; TITLE OF INVENTION: Proteins and nucleic acids NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell STREET: Ten South Wacker Drive, Suite 3000 CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 92
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
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INFORMATION FOR SEQ ID NO: 27:
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US-07-854-596B-27
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2055 AGAGTTTACTTACCATGTCAAAAATCGGGAACAAGCTTATGAGATCAATAAAAATCTGG 2114
                                                                                                           /note=
"OmpAL-Streptokinase-streptokinase fusion linked
by thrombin-cleavable VELQGVVPRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1395 IGTTAGCGTIGCTGGTACTGTTGAGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGA
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                                                                                                                                                                                                                                                                                                              Length 2589;
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                                                                                                                                                                                                                                                                                                             Score 1220.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                68.5%;
98.6%;
                                                                    NAME/KEY: misc_feature
LOCATION: 1..2589
OTHER INFORMATION: /note-
OTHER INFORMATION: "Ompal-
OTHER INFORMATION: by th.
PEATURE:
LOCATION: 4..2580
PEATURE:
NAME/KEY: mat_peptide
                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                  Matches 1231; Conservative
 STRANDEDNESS: single
                                   MOLECULE TYPE: CDNA PEATURE:
                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                           ; LOCATION:
US-07-854-596B-34
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GATCAAGAGTTTACTTACCATGTCAAAAATCGGGAACAAGCTTATGAGATCAATAAAAA 1032
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                                                                                                                           1093 AAAAAAGGGGAAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATC
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                                                                                                          AAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATC
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                                                                  1033 TCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTT
                                                                                                                                                                                 AAATACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,5968
FILING DATE: 03-JUN-1992
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
STATE: LL
SCOUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/07854596B
Patent No. 5434073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,33
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312-715-100
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
TYPE: nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-07-854-596B-34
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                16; Indels
                       NAME/KEY: misc_feature
LOCATION: 1..1257
OTHER INFORMATION: /note= "Methionyl-streptokinase
OTHER INFORMATION: fusion protein"
                                                                                                                                                                                                                                                                                                                                                         Score 1219.4; I
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.7%;
Matches 1229; Conservative (
                                                                                                                                                                                                                                                       ; NAME/KEY: mat_peptide
; LOCATION: 4..1248
US-07-854-596B-25
                                                                                                                                                                                                          4..1248
          MOLECULE TYPE: CDNA
                                                                                                                                                                                NAME/KEY: CDS
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FEATURE:
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ZIP: 60606

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UNY-1992
CLASSIFICATION: HOFORMATION:
NAMME: MCDORNALIN.
NAMME: MCDORNALIN.
NAMME: MCDORNALIN.
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
TELECOMMUNICATION INFORMATION:
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APPLICANT: Dawason, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
CORRESPONDENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: CLTY: IL
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US-07-854-596B-25
; Sequence 25, Application US/07854596B
; Patent No. 5434073
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                      /note= "OmpAL fused to mature
streptokinase gene"
                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                   68.4%; Score 1219.4;
Similarity 98.7%; Pred. No. 0;
29; Conservative 0; Mismatches
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LOCATION: 1..1317
OTHER INFORMATION:
OTHER INFORMATION:
PEATURE:
NAMEX KEX: CDS
LOCATION: 4..1308
PEATURE:
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US-07-854-596B-18
                                                                                                                                        NAME/KEY:
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                                                                                                 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1497
                                                                                                                                                                                                                                                         GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1617
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                                        847 GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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US-07-854-596B-18,
US-07-854-596B-18,
Sequence No. 5434073
GENERAL INFORMATION:
APPLICANT: pawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Dr. John J. McDonnell
Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTONNEY AGENT INFORMATION:
NAME: MCDONNEIL, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUICATION INFORMATION:
TELECOMMUICATION INFORMATION:
TELECOMMUICATION INFORMATION:
TELECOMMUICATION INFORMATION:
TELECOMMUICATION: 1312-115-1000
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1317 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
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STRANDEDNESS: single
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STATE: IL
COUNTRY: US
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                                                                                                                                                                                                        Score 1216.4;
Pred. No. 0;
0; Mismatches
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ilarity 98.7%;
Conservative
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                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 1226; Conserv
  FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
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GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 966
                                                                               GATGTCAACACCAACGAATTGCTAAAAAAGCGAGCAGCTCTTAACAGCGAACGTAAC
                                                                                                                                                                                TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAACATCTC
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                                                  GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
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fusion linked by Factor Xa-cleavable IEGR"
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ZIP: 60606
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UNN-1992
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MCDONNell, John J
REGISTRATION NUMBER: 26,949
REFERENCE DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATI
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APPLICANT: Hunter, Michael G
APPLICANT: Hunter, Michael G
APPLICANT: Caplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acid
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
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LOCATION: 1..1467
OTHER INFORMATION: /not
OTHER INFORMATION: fusi
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CITY: Chicago
STATE: 'IL
COUNTRY: USA
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AAGAATTTTTGCTAAGCGGACATGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAA
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     ACGGCAAGGTCTACTTTGCTGACAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCC
                       ACGCCAAGGTCTACTTTGCTGACAAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCC
                                                                          AAGAATTTTTGCTAAGCGGACATGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAA
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La Fuente
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APPLICANT: MAGRAZO, ISIS DEL Carmen APPLICANT: Garcia, Jose De Jesus De Japlicant: Ojalvo, Ariana Garcia
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                                                      TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
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Best Local Similarity 98.8%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 15;
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Patent No. 630973

GENERAL INFORMATION:

APPLICANT:

APPLICANT: Garcia, Jose De Jesus De La Fuente

APPLICANT: Garcia, Jose De Jesus De La Fuente

APPLICANT: Garcia, Jose De Jesus De La Fuente

APPLICANT: Menendez, Alina Seralena

APPLICANT: Becalona, Blder Pupo

APPLICANT: Griego, Martha De Jesus Gonzalez

TITLE OF INVENTION: STREFFOKINASE MITANTS

FILE REFERENCE: Sequence Listings 1-14 re: 976-5

PATEL NO. 6309873

CURRENT FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 11

LENGTH: 1209
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; ORGANISM: Streptococcus equisimilis
US-09-374-038-11
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US-09-374-038-11
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Best Local Similarity 98.8%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 15; Indels
APPLICANT: Menendez, Alina Seralena
APPLICANT: Escalona, Elder Pupo
APPLICANT: Becalona, Elder Pupo
APPLICANT: Masso, Ulio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14 re: 976-5
Patent No. 6413759
CURRENT APPLICATION NUMBER: US/09/658,179
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 1209
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US-09-658-179-11
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Sequence 38, Appl
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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-741-601-78
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## ALIGNMENTS

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SCHEKALL INFOCRATION:

SCHEKALL INFOCRATION:

APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: WUMBER: Us/09/940,235
CURRENT APPLICATION NUMBER: Us/09/940,235
CURRENT APPLICATION NUMBER: 1999-12-23
FRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SEQ ID NOS: 28
SEQ ID NOS: 28
TENATE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 0;
Live 0; Mismatches
                         ; Sequence 11, Application US/09940235; Publication No. US20030059921A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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GRENEAL INFORTATION:
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APPLICANT: Sahni, Girish
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APPLICANT: Roy, Chait
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APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
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CURRENT APPLICATION NUMBER: 109/411,349
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FRAESEQ for Windows Version 4.0
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Sequence 1, Application US/09940235

Sequence 1, Application US/09940235

Sequence 1, Application No. US20030059921A1

Sequence 1, Application No. US20030059921A1

Septicant: Namar. Rajesh

APPLICANT: Runar. Rajesh

APPLICANT: Rajespal, Kammara

APPLICANT: Rajespal, Kammara

APPLICANT: Rajespal, Kammara

APPLICANT: Rajespal, Kammara

APPLICANT: Sundaram, Vasudha

APPLICANT: Sundaram, Vasudha

APPLICANT: Yadav, Mahavir

ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINGEN ACTIVATION

ITILE REPERENCE: 07064-009002

CURRENT APPLICATION NUMBER: US/09/940,235

CURRENT FILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-12-23

PRIOR FILING DATE: 1998-12-24

NUMBER OF SEQ ID NOS: 28

SEQ ID NO:

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                                                                                             DB 3; Length 1377;
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                                                                                           Query Match 69.9%; Score 1245; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1245; Conservative 0; Mismatches
               ; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
US-09-940-235-5
LENGTH: 1377
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Sequence 6, Application US/09940235
Publication No. US20030059921A1
GENERAL INPORMATION:
APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram
APPLICANT: Su
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99.4%; Pred. No. 0;
iive 0; Mismatches
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; ORGANISM: Streptococcus equisimilis
US-09-940-235-6
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Best Local Similarity 99.4'
Matches 1237; Conservative
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                                                                        241 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC
                                                                                                                            ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
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RESULT 5 US-09-940-235-6

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ORGANISM: Artificial Sequence
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Publication No. US203005921A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Runar, Rajesh
APPLICANT: Radar, Malani, Girish
APPLICANT: Radar, Mahavir
APPLICANT: Radar, Mahavir
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadar, Mahavir
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION OF SAID
TITLE OF INVENTION UNMBER: US/09/940,235
CURRENT PRIJNG DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 1N 3825/DEL/98
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 10
SEQ ID NO 10
TITLES
TYPE: DNA
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                                            TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
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                                                                                              Length
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                                                                                       Score 1150.2;
Pred. No. 0;
0; Mismatches
OTHER INFORMATION: Hybrid cassette
                                                                                       Query Match 64.5%;
Best Local Similarity 99.7%;
Matches 1152; Conservative
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                                                                                                                       AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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Publication No. US20040236072A1
GENERAL INFORMATION:
APPLICANT: Olmsted, Stephen
APPLICANT: Applicant: Applicant: Nickbarg, Elliot
APPLICANT: Nickbarg, Elliot
APPLICANT: Nickbarg, Elliot
APPLICANT: Winter, Lourie
TITLE OF INVENTION: SURREAGE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REPERENCE: AM 100399
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JUNEARLY ENDINGATION

JUNEARLY SANI, Girish

APPLICANT: Sahni, Girish

APPLICANT: Rajagopal, Kammara

APPLICANT: Rajagopal, Kammara

APPLICANT: Rajagopal, Kammara

APPLICANT: Suddaram, Vasudha

APPLICANT: Suddaram, Vasudha

APPLICANT: Yadav, Mahavir

TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

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                         GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                       1203 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
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Publication No. US20030059921A1
GENERAL INFORMATION:
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                                                                                                                  1038 CTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chinnaiyan, Arul M.
APPLICANT: Rubin, Mark A.
APPLICANT: Rubin, Mark A.
APPLICANT: Sreekumar, Arun
TITLE OF INVENTION: Expression Profile of Prostate Cancer
FILE REPERENCE: UM-07221
CURRENT APPLICATION NUMBER: US/10/210,120
CURRENT PILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR PILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin Version 3.2
SEQ ID NO 49
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Pred. No. 2e-55;
0; Mismatches 32;
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Sequence 49, Application US/10210120
Publication No. US20030175736A1
GENERAL INFORMATION:
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79.8%;
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Best Local Similarity 79.8
Matches 308; Conservative
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                                                                                                                                                                    Score 1081.2; DB 8;
Pred. No. 1.3e-299;
0; Mismatches 103;
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SEQ TWARE: Patentin version 3.0
SEQ ID NO 657
LENGTH: 1323
                                                                                                 ; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-10-474-792-657
                                                                                                                                                                 Query Match 60.7%;
Best Local Similarity 91.7%;
Matches 1143; Conservative
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERBNCE: CLOOLSOO
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                         Length 2127;
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                                                                                                                                                                                                   Score 232.8; DB 9;
Pred. No. 2e-55;
0; Mismatches 32;
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           CURRENT APPLICATION NUMBER: US/10/909,035
CURRENT FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.2
SEQ ID NO 49
LENGTH: 2127
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                                                                                                                                                                                                       13.1%;
79.8%;
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Best Local Similarity 79.8
Matches 308; Conservative
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Matches 308; Conservative
FILE REFERENCE: UM-09098
                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-909-035-49
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CORGANISM: Homo sapiens
US-10-741-601-70
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                                                                                                                                                                                                             Sequence 4288, Application US/10956157
Publication No. US20050118625A1
Publication No. US20050118625A1
APPLICANT: Wyeth
APPLICANT: Mounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 10.081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICANTON NUMBER: 2004-10-04
NUMBER OF SEQ ID NOS: 318965
SOFTWARE: Patentin version 3.2
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             AGCGGATCTGGCCCCTTCACCGATGTTCGTTGCTGGACCTGAGTGGCTGCTAGACCGT
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Pred. No. 2e-55;
0; Mismatches 32;
                                                                                     CCATCTGTCAACAGCCAATTGGT 593
                                                                                                                        CAGCCTCCTATGCCCACTGTGT 982
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Publication No. US20050136493A1
GENERAL INFORMATION:
APPLICANT: Chinnalyan, Arul M.
APPLICANT: Lawman, Bharathi
APPLICANT: Teekumar, Arun ITLE OF INVENTION: AMACR Cancer Markers
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ilarity 79.8%;
Conservative
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Best Local Similarity
Matches 308; Conserv
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US-10-956-157-4288
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-10-956-157-4288
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LENGTH: 2127
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US-10-909-035-49
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-75
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US-10-741-600-244
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LENGTH: 2488
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| Publication No. US20050026169A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al.
| TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
| FILE REFERENCE: CL001499
| CURRENT APPLICATION NUMBER: US/10/741,600
| CURRENT FILING DATE: 2003-12-22
| NUMBER OF SEQ ID NOS: 73997
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 238
| LENGTH: 2443
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973 TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC 1032
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                                                         1033 GGACGCATCACTTCTAGAAATAGATGCAACGATCAGGACACAACCATCA
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Pred. No. 2.1e-55;
0; Mismatches 32;
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Best Local Similarity 79.8%;
Matches 308; Conservative (
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; ORGANISM: Homo sapiens
US-10-741-600-238
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Sequence 244, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION: US20050026169A1
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                  APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERBNCE: CLOOLSOO

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE: RestSEQ for Windows Version 4.0
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Pred. No. 2.1e-55;
0; Mismatches 32;
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; Sequence 75, Application US/10741601; Publication No. US20040166519A1; GENERAL INFORMATION:
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Best Local Similarity 79.8%;
Matches 308; Conservative
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973 TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC 1032
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                                                                                                                                          328 GGACGCATCACTTCCACTTCTAGAAATAGATGCAACGATCAGGACAAAGACACATCCTAT 387
                                                                        ----TGGGAGAAGGCAGC 327
                   46;
Query Match
Best Local Similarity 79.8%; Pred. No. 2.1e-55;
Matches 308; Conservative 0; Mismatches 32; Indels 46;
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Search completed: February 1, 2006, 14:21:21 Job time : 1474.42 secs

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January 31, 2006, 18:17:59; Search time 329.469 Seconds (without alignments) 4492.841 Million cell updates/sec
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1782
1 tcgcttcacgttcgctcgcg.....ataaccctaacgacaaataa 1782
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/ Ggn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6059551 seqs, 415333918 residues
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Listing first 45 summaries
                                                                                                                   - nucleic search, using sw model
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	, Appl	Appl	Appli	Appli	Appli	, Appl	Appli	14, App	٠.,		7, App	1, App	3, App	8, App	104, App	6, App	7, App		106, App	O, App	109, App	3, Appli
Description	Sequence 11	Sequence 12	Sequence 5,	Sequence 1,	Sequence 6,	Sequence 10	Seguence 9,	_	_	Sequence 11	Sequence 11	Sequence 11	Sequence 11	Sequence 10	٠.	Sequence 11	Sequence 10	Sequence 693		Sequence 11		Sequence 3,
SUMMARIES ID	US-10-631-558-11	US-10-631-558-12	US-10-631-558-5	US-10-631-558-1	US-10-631-558-6	US-10-631-558-10	US-10-631-558-9	US-10-995-561-114	US-10-995-561-105	US-10-995-561-112	US-10-995-561-117	US-10-995-561-111	US-10-995-561-113	US-10-995-561-108	US-10-995-561-104	US-10-995-561-116	US-10-995-561-107	US-10-821-234-693	US-10-995-561-106	US-10-995-561-110	US-10-995-561-109	US-10-631-558-3
DB	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
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Query Match	100.0	94.5	6.69	69.8	69.1	64.5	63.6	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	12.8
Score	1782	1684	1245	1243.4	1232.2	1150.2	1134.2	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	228
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	Sequence 2446, Ap	Sequence 416, App	Sequence 416, App	Sequence 72, Appl	Sequence 72, Appl	Sequence 14, Appl	Sequence 15, Appl	17,	Sequence 18, Appl	13,	14,	67,	H	8	Sequence 1, Appli	Sequence 43, Appl	Sequence 33, Appl	Sequence 1, Appli	Sequence 254, App	17, 7	86,	Sequence 87, Appl
US-10-995-561-13237		US-11-009-840A-416	US-11-009-873A-416	US-11-009-840A-72	US-11-009-873A-72	US-10-742-634-14	US-10-742-634-15	US-11-106-820-17	US-11-106-820-18	US-11-106-820-13	US-11-106-820-14	US-11-017-550-67	US-10-519-531-1	US-10-519-531-8	US-11-230-995-1	US-10-966-483-43	US-11-021-441-33	US-11-209-589-1	US-10-623-155-254	US-11-094-586-17	US-11-076-733-86	US-11-076-733-87
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## ALIGNMENTS

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Sequence 11, Application US/10631558
Sequence 11, Application US/10631558
Sequence 11, Application US/10631558
Sequence 11, Application No. US208500260598A1
GENERAL INFORMATION:
APPLICANT: Raigesh
APPLICANT: Raigespal, Kammara
APPLICANT: Raigespal, Kammara
APPLICANT: Raigespal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION UNMERR: US/09/940,235
FRIOR FILING DATE: 1099-12-23
FRIOR FILING DATE: 1099-12-24
NUMBER OF SEQ ID NOS: 28
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: DNA
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i Sequence 5, Application US/10631558

i Publication No. US20050260598A1

i GENERAL INFORMATION:

i APPLICANT: Rumar, Rajesh

i APPLICANT: Rajagopal, Kammara

APPLICANT: Rajagopal, Kammara

APPLICANT: Sundaram, Vaeudha

i APPLICANT: Sundaram, Vaeudha

i APPLICANT: Yadav, Mahavir

i TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE

TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAY

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEIN

FILE REFERENCE: 07064-009002

CURRENT APPLICATION NUMBER: US/10/631,558

CURRENT FILING DATE: 2002-07-31

PRIOR FILING DATE: 2002-04-09
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                                                           Length 2096;
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                                                         Score 1684; DB
Pred. No. 0;
0; Mismatches
                cassette
                                                                                   0;
                                                      Query Match
Best Local Similarity 99.7%;
Matches 1687; Conservative
            OTHER INFORMATION: Hybrid US-10-631-558-12
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FEATURE:
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1557 1152 1617 1212 1677 1272 1737 1332

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Sequence 1, Application US/10631558

Publication No. US2005260598A1

Sequence 1, Application US/10631558

Publicant Numar, Rajesh

APPLICANT: Kumar, Rajesh

APPLICANT: Sahni, Girish

APPLICANT: Rajagopal, Kammara

APPLICANT: WOULD CLOT-SPECIFIC STREPTOKINASE

ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

FULE REFERENCE: 07064-009002

CURRENT FILING DATE: 2003-07-31

PRIOR PLING DATE: 1999-12-23

PRIOR PLING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1245

TVENT PLANDER

LENGTH: 1245

TVENT PAPEL TATES
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   GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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                                                            GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                 1033 GATGTCGATACCAACGAATTGCTAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                        TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATTCTC
                                                                                                                                                                         1093 Tragacticagagartraracgarccrcgrgaraaggcraaacracrcracaacaarcrc
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99.9%; Pred. No. 0;
ive 0; Mismatches
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Matches 1244; Conservative
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US-10-631-558-1
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                                                                                                                                                                                                                                  Length 1377;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1245; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1377
                                                                                                                                                                       ORGANISM: Streptococcus equisimilis US-10-631-558-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                              658
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GENERALI INFORMATION:

APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Rayiagopal, Kammara
APPLICANT: Rayiagopal, Kammara
APPLICANT: Rayiagopal, Kammara
APPLICANT: Rayiagopal, Kammara
APPLICANT: Sundaram, Vasudha
TITLE OF INVENTION: PROTEINS POSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: SUNGARE: US/10/4-03
FRIOR APPLICATION NUMBER: US/09/940,235
FRIOR APPLICATION NUMBER: 10/4-10/3-12-23
FRIOR FILING DATE: 1099-12-23
FRIOR PILING DATE: 1099-12-23
FRIOR FILING DATE: 1999-12-24
FRIOR FILING DATE: 1999-12-24
FRIOR FILING DATE: 100-10-24
FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR FRIOR 
          1141 CATTTAGCCTATGATAAGATCGTTATACCGAAGAAGAACGAGAAGTTTACAGCTACCTG 1200
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; ORGANISM: Streptococcus equisimilis
US-10-631-558-6
                                                                                                                                                                                       Sequence 6, Application US/10631558; Publication No. US20050260598A1; GENERAL INFORMATION:
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Pred. No. 0;
CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/99/940,235
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PSECSER FOR WINDOWS VERSION 4.0
SCOFTWARE: PSECSER FOR WINDOWS VERSION 4.0
LENGTH: 1661
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Publication No. US20050260598A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sahni, Girish
APPLICANT: Rajespal, Kammara
APPLICANT: Rajespal, Kammara
APPLICANT: Rajespal, Kammara
APPLICANT: Vadav, Mahavir
APPLICANT: Yadav, Mahavir
ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
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Sequence 9, Application US/10631558
PUBLICANT NO. US200500560598A1
SEQUENCE INVORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Saini, Girish
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: NoreL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: REACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION UNMERR: US/09/940,235
PRIOR FILING DATE: 1099-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: DATE: NANA
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                                                                                                                                                                                                1023 GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                         GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                                                                                                                                                          GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                  TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAACTACTACAACAATCTC
                                                                  GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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ORGANISM: Artificial Sequence
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US-10-631-558-9
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1033 GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACACACCATAT 1092
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRAESEQ for Windows Version 4.0
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                                                                                                          DB 7;
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Pred. No. 2.3e-59;
0; Mismatches 32
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                                                                                                        13.1%;
                                                                                                                                                         Matches 308; Conservative
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ORGANISM: Homo sapiens
                                 ORGANISM: Homo sapiens
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; ORGANISM: Homc
US-10-995-561-105
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US-10-995-561-112
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Best Local &
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Best Local 9
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                                                                                             RESULT 8

US-10-995-561-114

Sequence 114, Application US/10995561

Sequence 114, Application US/1099561

Publication No. US20050272054A1

GENERAL INFORMATION:
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF

CURRENT APPLICATION UNMBER: US/10/995,561

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 114

LENGTH: 2443
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Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 105
LENGTH: 2488
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Pred. No. 2.3e-59;
0; Mismatches 32;
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1173 CATTTAGCTGGTGGT 1187
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13.1%;
Best Local Similarity 79.8%;
Matches 308; Conservative
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ORGANISM: Homo sapiens
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US-10-995-561-105
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Publication No. US20050272054A1
GENERAL INFORMATION: US20050272054A1
GENERAL INFORMATION: GENERAL
TITLE OF INVENTION: GENERAL DESCRIBER AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THERROF FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FateSEQ for Windows Version 4.0
SEQ ID NO 113
LENGTH: 7935
                                                   APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOOISS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
SOFTWARE FALES FACES FOR WINDOWS 185702
SOFTWARE FACES FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 232.8; DB 7
Pred. No. 4.4e-59;
0; Mismatches 32
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     US20050272054A1
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Best Local Similarity 79.8
Matches 308; Conservative
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ORGANISM: Homo sapiens
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Publication No. US20
GENERAL INFORMATION:
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Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS FILE REPERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                         ACAGGCAACGGCCGAGGAGGGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG
AGAATTGGAGACACCTGGAGCAAGAAGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                   1093 AGAATIGGAGACACCIGGAGCAAGAAGGATAAICGAGGAAACCIGCICCAGIGCAICIGC
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Best Local Similarity 79.8%; Pred. No. 4.4e-59;
Matches 308; Conservative 0; Mismatches 32;
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US-10-995-561-111
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ORGANISM: Homo sapiens
US-10-995-561-117
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LENGTH: 7823
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPRENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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13.1%; Score 232.8; DB 7;
Best Local Similarity 79.8%; Pred. No. 4.5e-59;
Matches 308; Conservative 0; Mismatches 32;
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; ORGANISM: Homo sapiens
US-10-995-561-104
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US-10-995-561-104
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Publication No. US20050272054A1
GRNERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE REPRENTE; CLOUG1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING; DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: Fast$EQ for Windows Version 4.0
SEQ ID NO 108
LENGTH: 7959
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Pred. No. 4.5e-59;
0; Mismatches 32;
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ORGANISM: Homo sapiens
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US-10-995-561-108
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         GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Listing first 45 summaries
                                                      - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BX391752 BX391752	AL603368 DKFZp686C	AI095589 qb24a08.x	CN482442 hw20d08.y	CN419611 170005313	BM715855 UI-E-EJO-	_	BC100030 Homo sapi	CR749316 Homo Bapi	BX640608 Homo sapi	Homo	BX640875 Homo sapi	CD613789 56022208J	CD613788 56022208H	AU140971 AU140971	CR749317 Homo sapi	CN419585 170005318	AU140993 AU140993	CN419650 170005315	CN419649 170005315	BE009640 PM4-BN017	BQ292415 PM0-AN008
SUMMARIES	OI .	BX391752	AL603368	AI095589	CN482442	CN419611	BM715855	BC078656	BC100030	CR749316	HSM806653	CR749281	HSM806992	CD613789	CD613788	AU140971	CR749317	CN419585	AU140993	CN419650	CN419649	BE009640	BQ292415
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	Score	233.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	232.8	231.2	231.2	231.2	231.2	230.2	230.2	229.5	229.2	229.2	229.2
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BX327266 CM419631 BQ545197 BQ574857 AU140802 BF081716 AA376374 BF956982 AA682090 AL706215 AU140789 BQ3405767 BQ340576 BQ340575 BQ340676	ALIGNMENTS  943 bp mRN  13-PRIME, mRNA sequence  7701  Chordata, Craniati Euarchontoglires; Jessee, J. and Poli braries and normali braries and normali ux, CP 5706 - 91057  cope. Cns.fr, Web: primed with a Not: eye. Cns.fr, Web: primed with a Not: eye. Cns.fr, Web: primed with a Not: eye. This sequence  RCOR V sites of the  rary was constructed  m about this cluste e.cns.fr/cdna?s=CSS	/Qualifiers m="Homo sapiens" e="mANA" ="taxon:9606" CSOD1065Y122" CYPPE="PLACENTA of the sapien of the sapien of the sapien of the prime end of with Not I and the pCMVSPORT (	Score 233.8;
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	BX391752  BX391752 Homo sapiens PLACENTA (clone CSODIO65X122 3-PRIME, mRNJ BX391752.1 GI:30607701  BX391752.1 GI:30607701  BX391752.1 GI:30607701  BX391752.1 GI:30607701  Homo sapiens (human)  Contact: Guber, C., Jessee, J. ar  Whyll-length cDNA libraries and r  Unpublished (2001)  Contact: Genoscope - Centre National de S  Grane Gaston Cremieux, CP 5706  Email: seqref@genoscope.cns.fr,  1st strand cDNA was primed with  end enriched, double-strand cDNA  into the Not I and EcoR V sites  was normalized. Library was cone  division of Invitrogen. This sec  division of Invitrogen. This sec  for more information about this	Location/Qualifiers 1. 943 /organism="Homo sapie: /organism="Homo sapie: /db_xref="taxon:9606" /db_xref="taxon:9606" /clone="CSDD1065Y122" /clone="Type="FLACENT. /clone lib="Homo sapi: /note="lst strand cDN primer. Five prime en digested with Not I a sites of the pCMVSPOR	13.1%;
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                                                                                                                                                         db24a08.x1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:1697174 3' similar to gb:x02761_cds1 FIBRONECTIN PRECURSOR (HUMAN);, mRNA sequence.
A1095589.1 GI:3434565
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
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Unpublished (1997)
Contact: Roberts Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1871 Std Error: 0.00
Seg primer: -40013 fwd. ET from Amersham
High quality sequence stop: 446.
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1 (bases 1 to 465)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                    254 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG
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                                                                                          Gaps
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                                                Length 451;
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                                         13.1%; Score 232.8; DB 1; 79.8%; Pred. No. 3.7e-55; ive 0; Mismatches 32;
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/lab_host="DH10B"
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DKF22686C067_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
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Hominidae, Homo.

Tobases I to 451)

Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.

EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the 5' sequence of the Clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  German Genome Project.

No sl sequence available.

This clone (DKFZp688C067) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
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                                                                 254 CCCATAGCTGAGAAGTGTTTTGATCATGCTGGTGGGACTTCCTATGTGGTCGGAGAAACG
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Pred. No. 2.4e-55;
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  80.08;
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oligo(dT) primer [5,
AACTGGAAGAATTCGGGCCGCCTTTTTTTTTTTTTTTT 3.],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                621 bp mRNA linear EST 26-APR-2004 hw20608.y1 Human primary human ocular pericytes. Unamplified (hw) CN482442. CN482442.1 GI:46563946
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Tsai,J.Y. and Wistow,G.
Expressed sequence tag analysis of cultured primary human ocular
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                            13.1%; Score 232.8; DB 1; Length 465; larity 79.8%; Pred. No. 3.7e-55; Conservative 0; Mismatches 32; Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2004)
Contact: Wistow G
Sction on Molecular Structure and Functi
National Bye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABI)
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Plate: 20 row: d column: 08
Seq primer: MJ3RP1 reverse primer
Location/Qualifiers
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/mol_type="mRNA"
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Homo sapiens
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Fax: 301 496 0078
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Matches 308; Conserv
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/note="Organ: Eye; Vector: pSportl; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSPORTI vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGAGTAGTTCAGAGGGGCGCC(T)15-3']. CDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
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5', mRNA sequence.
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1 (bases 1 to 626)

Enadenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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                                                                                /dev_stage="Adult"
/lab_host="EMDH10B".
/clone lib="Human primary human ocular pericytes.
UnamplIfied (hw)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
13.1%; Score 232.8; DB 7; Length 621;
Best Local Similarity 79.8%; Pred. No. 4e-55;
Matches 308; Conservative 0; Mismatches 32; Indels 46
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17005313190699 GRN_EB Homo sapiens cDNA
CN419611 GI:47407205
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                                                       cell_type="pericytes"
db_xref="taxon:9606"
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Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="UI-E-EJO-ahj-h-11-0-UI"
/tissue type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 AGGGBATCTGGCCCTTCACCGATGTTCGTATTGCTGGACCTGAGTGGCTGCTAGACCGT
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                                                                                                    MEBRF, Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 232.8; DB 3; Length 765;
Pred. No. 4.3e-55;
0; Mismatches 32; Indels 46;
                                                            for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                     l. .765
'organism="Homo sapiens"
  Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:9606"
                                                                             University of Iowa
375 Newton Road, 4156 MEBRE,
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      mol_type="mRNA"
                                                              Coordinated Laboratory
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                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tiskue_type="embryonic stem cells, embryoid bodies
/diskue_type="embryonic stem cells, embryoid bodies
/clone_lib="GRN_EB"
/clone_lib="GRN_EB"
/note="foligo dT_primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508 AGCGGATCTGGCCCCTTCACCGATGTTGTTGCTGGACCTGAGTGGCTGCTAGACCGT 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 AGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCC 429
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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1 (Dases 1 to 765)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - TGGGAGAAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 232.8; DB 7; Length 626; llarity 79.8%; Pred. No. 4.1e-55; Conservative 0; Mismatches 32; Indels 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                   Regenerative Medicine
Geron Corporation
233 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                               Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 cagcciccrccrargeccarigner 455
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                                                                                                                                   Email: rbrandenbergerengeron.com
Insert Length: 626 Std Error:
Location/Qualifiers
                       Contact: Brandenberger R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM715855
BM715855.1 GI:19029113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308;
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Best Local S
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KEYWORDS
SOURCE
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AUTHORS
TITLE
PUBMED
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BM715855
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                    COMMENT
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241 313

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Gaps

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Length 7501; IndelB 327

985 447

387

DEFINITION

RESULT 7 BC078656

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE

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Rammaniae; Homo.

Hominidae; Homo.

Straubsberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collinns, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max. S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mallek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Mizny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1046 ACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGCCACCATCG 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC100030 7501 bp mRNA linear HTC 02-AUG-2005 Homo sapiens cDNA clone IMAGE:30343682, containing frame-shift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          806 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGGGAGAAAGG 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 866 TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC 925
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 CCCATAGCTGAGAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG
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/db_xref="taxon:9606"
/clone="INAGE:30347017"
/tissue_type="Placenta, normal"
/clone_lib="NIH MGC_147"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                  Score 232.8; DB 4
Pred. No. 8.6e-55;
                                                                                                                                                                                                              /note="Vector: pBluescriptR"
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 79.8%;
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 -----
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Homo sapiens
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BC100030
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1. (bases 1 to 7501)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Mang, J., Hsich, F.,
Botacherko, L., Marusina, K., Barmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Todellano, N.A., Peters, G.J.,
Abramson, R.D., Mallahy, S.J., Gunellano, N.A., Peters, G.J.,
McKerhan, K.J., Mallahy, S.J., Gunellano, N.A., Peters, G.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D. K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B.,
Schnerzch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                           BC078656 1501 bp mRNA linear HTC 21-JUL-2005 Homo sapiens cDNA clone IMAGE:30347017, containing frame-shift
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: Chicken, harty://www-shgc.stanford.edu
Contact: (Dickson, Mark) med@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found
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482 AGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Submitted (02-AUG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
mail: cgapba-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael Brownstein / Ted Usdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                              CAGCCTCCCTATGCCACTGTGT 567
                                                                568 CCATCTGTCAACAACAGCCAATTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                               BC078656.1 GI:50925326
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 7501)
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AUTHORS CONSRIM TITLE JOURNAL

REMARK

COMMENT

PUBMED REFERENCE JOURNAL

CONSRIM

TITLE

/organism="Homo sapiens"

source

PEATURES

567

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GGYMLECVCLGNGGGEWTCKP I AERCFPHAAGTS YVORETWEEPYGGAMMYDCTCLGE
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NYDADQKGFRCPMAAHEEI CTTNGGWYRTGIGDWGDHWGHARCCTVGWGRGEWTC
TAYSQLABQCTVDD TTYNVNDTFHKRHEBGHNLNCTCFGGGRGRWCDPVDQCQDSET
GTFYQIGDSWEKYVHGYRYQCYCYGRGIGEWTCTCYGGGRGRWCDPVDQCQDSET
GTFYQIGDSWEKYVHGYRYQCYCYGRGIGEWTCTTFFFBSQPN
SIPQIQHGBYRPPGTTTSTSTPYTSTFFYTTSTFGAT
VSASDTVSGFRVETESEGDBPQYLDLPSTATSNIIPDLLPGRKYTINNYQISBDGE
                                                                                                                                                           CR749316 7777 bp mRNA linear HTC 19-AUG-2004
Homo sapiens mRNA; cDNA DKFZp686K08164 (from clone DKFZp686K08164).
CR749316
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NLPETANSVTLSDLQPGVQYNITIYAVERNQESTPVVIQQETTGTPRSDTVPSPRDLQ
PVEVTDVKVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPISRNTFAEVTGLSPGVT
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hlcc3). Vector pSport1_Sfi; host
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VSQSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESKPEAEETCFDKYT
GNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRPHET
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VGLTRRGQPRQYNVGPSVSKYPLRNLQPASBYTVSLVAIKGNQESPKATGVPTTLQPG
SSIPPYNTEVTETTIVITWTPAPRIGFKLGVRPSQGGBAPREVTSDSGSIVVSGLTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686K08164
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuherberg, (GERMAN) MISS, ingolsecence Leansell, Description of the form S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKPZ); Email S. Wiemann@dKz-heidelberg.de, sequenced by BWFZ (Blomedial Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp686K08164) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.
1 (bases 1 to 7777)
Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/note="fibronectin 1, differentially spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
/protein_id="CAH18171.1"
/db_xref="G1:51476362"
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/clone_lib="686 (synonym: hlcc3
DH10B; sites SfiIA + SfiIB"
     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="DKFZp686K08164"
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/gene="DKFZp686K08164"
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/db_xref="taxon:9606"
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
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                                                                                                                                                                                LOCUS
                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 198 Row: j Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 47132556
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1045
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                                                                                                                                                                                                                                                          Direct Submission
Submission
Submission
Submission
Gene Collection (MGC). Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael Brownstein / Ted Usdin
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:30343682"
/tissue type="Placenta, n
/clone_lib="NIH MGC_147"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                     AUTHORS
CONSRIM
TITLE
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COMMENT
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Homo sapiens mRNA; cDNA DKFZp686M04163 (from clone DKFZp686M04163).
BX640608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDNGVNYKIGEKWDRGGENGQMMSCTCLGNGKGEFKCDPHEATCYDDGKTYHVGEQWQ
KEYLGAICSCTCFGGGRGWRCDNCRRPGGEPTPEGTTGGSYNQYSQRYHQRTNTNVNC
PIECFWPLDVQADREDSRE"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Blocker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
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Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764
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Pred. No. 8.7e-55;
); Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="UniProt/TrEMBL:Q6N0A6"
/translation="MLRGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVA
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QTTSSGSGPPTDVRAAVYQPQPHPQPPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCT
CLGNGVSCQETAVTQTYGGNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNY
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TVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTD
VQGNSISVKWLPSSSPVTGYRVTTPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVV
Neuherberg, German, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Cesearch Cotter (DKFZ); Bmail s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRRARVTDATETTITISWRTKTETITGRQVDAVPANGQTPIQRTIKPDVRSYTITGLQ
PGTDYKIYLYTLNDNARSSPVVIDASTAIDAPSNLRFLATTPNSLLVSWQPPRARITG
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                                                                                                                                                                                                                                                                                             Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Blease contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686M04163 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                      German Genome Project.
This clone (DKFZp686M04163) is available at
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/protein_id="CAR45114.1"
/db_xref="G1.34364617"
/db_xref="G0A:Q6N006"
/db_xref="G0A:Q6N006"
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|mol_type="mRNNA"
|db_xref="RZPD:DKF2p666M04163Q"
|db_xref="taxon:9606"
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|db_xref="InterPro: IPR002086"
|db_xref="InterPro: IPR003961"
|db_xref="InterPro: IPR006209"
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/note="fibronectin precursor"
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/gene="DKFZp686M04163"
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                PNASTGGRALSQTTISWAPPQDTSEYIISCHPVGTDBEPLQFRVPGTSTSATLTGLTR
GATYMIVBALKDQQRHKVREEVVTVGNSVNEGLNQFTDBCFDPYTYSHYAVGDEWE
RWSESGFKLLCQCLGFGSGHPRCDSSRWCHDNGVNYKIGEKWDRQGENGQWMSCTCLG
NGKGBFKCDPHEATTCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQGRGWRCDNCRRPGG
EPTPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQADREDSRE"
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Homo sapiens mRNA; cDNA DKFZp686F10164 (from clone DKFZp686F10164).
CR749281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1047 ACAGGCAACGGCCGAGGAGAGTGGAAGTGTAGAGGCACACCTCTGTGCAGACCACATCG 1106
QMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGEBIQIGHIPREDVDYHLYPHGPGLN
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686F10164
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Blomedical Research Center at the
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1 (bases 1 to 7885)

Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.

The German CDIA Consortium
Direct Submission
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                                                                                                                                                                                                                                                                                                          807 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGCTGGGGACTTCCTATGTGTGGGAGAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                       867 TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGGCATCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
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                                                                                                                                                                                   Length 7868;
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                                                                                                                                                                                   Score 232.8; DB 4;
Pred. No. 8.7e-55;
); Mismatches 32;
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                                                                                                                                                                                   13.1%;
ilarity 79.8%;
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                                                                                                                                                                                     Query Match
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HESTPLAGGORTGLDS PTGIDPSDITANSFTVHNIAPRATITGYRIRHHPEHFSGRER
EDRVPHSKNSITLTNLFPGFTEYVVSIVALNGRESPLLIGQOSTVSDVPRDLEVVAAT
PTSLLISWDARAVTWRYRITYGETGGNSPYQBFTVPGSKSTATISGLKEGWDYTITY
YAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNSISVKMLPSSSPVTGYRVTIT
TPKNGFCPFTKKTRGFDQTEWTIEGLQPTVEYVSYVANPSGESQPLVQTAVTITP
PTDLKFTQVTPTSLSAQWTPBNVQLTGYRWVTPKEKTGPMKEINLAPDSSSVVVSGI
WVATKKEVSYYALKOTILTSRPAGGVTTLENVSPPRRAVTDATETTITISWFKKTET
ITGFQVDAVPANGQTPIQRITKPDVALTLENVSPPRRAVTDATETTITISWFKKTET
ITGFQVDAVPANGQTPIQRITKPDVALTLENVSPPRRAVTDATETTITISWFKKTET
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OPPPGRINSKUDNRGNLLQCICTGNGRGEWKCERHTSYGTTSGGSGPFTDVRAAVYQPQPH
OPPPGRICVTDSGVVSVGWOWLKTGONROMELTCTCLGNGVSCOETAVTQTYGGNSNGE
PCVLPPTYNGRYFYSCATEGRODGHJMCSTTGNYEQDQXYSFCTDHTVLVQTRGGNSNG
GALCHPPLYNGRYFSCATEGRODGHJMCSTTGNYEQDQXYSFCTDHTVLVQTRGGNSN
GALCHPPLYNDHNCHPMCHPMCSTTGNYEDADQKFGFCPMAAHEEICTTN
KWHREGHMLMCTCFGCGRGRWKCDPVDQCQDSETGTFFYQIGDSWEKYYHGVRYCYCYC
GRGIGEWHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQWNAPQPSHISKYILRWRPR
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PRPYPPNVGQBALSQTTISMAPRQDTSEYIISCHPVGTDEEPLGFRVEGTSTSATLIG
LTRGATYNIIVBALKOQRHKVREEVVTVGNSVTGINQPTDBSCPPPYTVSHYAVGD
EWERNSESGFKLLCCCLGFGSGHFRCDSSRWCHDNGYNYKIGEKWDRQGENGQMNSCT
CLGNGKGEFKCDPHEATCYDDGKTYHVGEQWQKSYLGAICSCTCFGGGRGWRCDNCRR
                                                                                                                                                                                                                                                                                      /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MAGGPRRLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPVP
PPTLWPPPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNMLRGPGPGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERT
YLGNALVCTCYGGSRGFNCESKPEAEETCPDKYTGNTYRVGDTYERPKDSMIWDCTCV
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                                                                                                                                                                                                                               primary cell culture"
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                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/note="fibronectin 1, differentially spliced"
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79.8%; Pred. No. 8.7e-55;
tive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="hypothetical protein"
/protein_id="CAH18136.1"
/db_xref="G1:51476292"
                                                                                                                                                                                                                                      /tissue_type="uterus endothel,
organism="Homo sapiens"
                                                      ol_type="mRNA"
o_xref="taxon:9606"
lone="DKFZp686F10164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="DKFZp686F10164"
30. .7103
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1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSM806992 8411 bp mRNA linear HTC 23-FEB-2005
Homo sapiens mRNA; cDNA DKFZp68601166 (from clone DKFZp68601166).
BX640875
                                                                                                                                                                                                                                                                                      1146 AGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCC 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="RXPD:DKFZp686011660"
/db_xref="caxon:9606"
/db_xref="caxon:9606"
/clone="DKFZp68601166"
/tissue type==ndometrium carcinoma cell line"
/clone_lib="686 (synonym: hlcc3). Vector pSportl_Sfi; host DH108; sites SfilA + SfilB"
                                                                                                                                                               507
                                                                          447
                                                                                                                                                                                                                                              508 AGCGGATCTGGCCCCTTCACCGATGTTCGTATTGCTGGACCTGAGTGCTAGACCGT 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Research Center (DKPZ); Bmail s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Genome Project.

This clone (DKFZp68601166) is available at the RZPD Deutsches Ressourcentzentrum fuer Genomiforschung GmbH in Berlin, Germany. Please contact RZPD for ordering://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp68601166 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

Location/Qualifiers

1. 8411
//crganism="Homo" sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-FEB-2005) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERWANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                                                                                                  1026 AGAATTGGAGCACCTGGAGCAAGAAGATAATCGAGGAAACCTCCTCCAGTGCATCTCC
                                                                                                                                                                                        1086 ACAGGCAACGGCCGAGGAGAGGGGGAAGTGTGAGAGGCACACACTCTGTGCAGAGACACACTCG
                                                                     AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                                                                                                                          ACAGGCAACGCCGAGGAGAGTGGAAGTGTGAGAGGCACACATCTGTGCAGACCACATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="hypothetical protein"
/protein id="CAE45932.1"
/db_xref="G1:34365170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |db_xref="GOA:Q6MZU5"
|db_xref="InterPro:IPR000083"
|db_xref="InterPro:IPR000562"
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                                                                                                                                                                                                                                                                                                                                 568 CCATCTGTCAACAACAGCCAATTGGT 593
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/note="fibronectin 1"
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/db_xref="UniProt/TremBL:Q6MZU5"
/translation="MLRGPGPGILLLAVICLGTAVPSTGASKSRRQAQQWVQPGSPVA
VSQSRPGCYDNGKHYQINQQMETYILGNALVCTCYGGSRGFNCESKPEAEBTCFDKYT
GNTYRVGDTYBRRPGSMIWDCTCIGAGRGRISCTIANRCHEGGGGSYKIGDTWRRPHET
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GSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCERHTSV
QTTSSGSGPPTDVRAAVYQPQPHPQPPPYGHCVTDSGVVSSVGMQMLKTQGNKQMLCT
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SODOXYSTCTUHTVLVQTRGASNGALCHPFFTYNHNYTYDTGTSGRENDNKWGCTTQ
NYDADQKFGFCPMAHEBICTTUNGVNYRIGDQMDKQIDMGHMRCTCVGNGEBWTC
IAYSQLRDQCIVDDITYNVNDTFHKRHEBGHMLNCTCFGQGRGRWKCDPVDQCQDSET
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SIQQYGHQEVTRFDFTTTSTSTPVTSNTVTGETTPFSPLVATSESVTEITASSFVVSW
VSASDTVSGFRVEXELSEEGDEPQYLDLPSTATSVNIPDLLPGRKYIVNVQISEDGE
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YTITGLOPGTDYKI YLYTLADNARSS PVVIDASTAIDAPSNIRFLATTPNSLLVSWOP
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PGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFTQVTPTSLSAQMTPPNVQLTG
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MSCTCLGNGKGEFKCDPHEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCD
NCRRPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNYPIECFMPLDVQADREDSRE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 GGACGCATCACTTGCACTTCTAGAATAGATGCAACGATCAGGACACAAGGACATCCTAT 387
                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACAACAAGGACATCCTAT
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                                                                                                                                                                                                                                           Hominidae, Homo.

1 (bases 1 to 551)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 551;
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                                                             CD613788 551 bp mRNA lines
56022208H1 FLP Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="texton:9606"
/clone lile="FLE"
/note="Vector: pDrive Cloning Vector"
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Pred. No. 1.1e-54;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                         Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .551
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: gfu@incyte.com.
Location/Qualifiers
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AU140971.1 GI:11002492
                                                                                                                        CD613788.1 GI:40262052
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                                                                                                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 307; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 CCCATAGCTGAGAAAGTGTTTTTGATCATGCTGCTAGGACTTCCTATGTGGTGGAGAAACG 381
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508 AGCGGATCTGGCCCCTTCACCGATGTTCGTATTGCTGGACCTGAGTGGCTGCTAGACCGT 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 -----TGGGAGAGGCAGC 327
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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1 (Dasses 1 to 548)

Fu,G.K., Wang,J.:, Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)
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                                                                                                                                                                                                                          linear
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56022208J1 FLP Homo sapiens cDNA, mRNA sequence
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA 94304,
                                                                                                       1168 CAGCCTCCTCTATGCCCACTGTGT 1193
                                                                                568 CCATCTGTCAACAACAGCCAATTGGT 593
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3160 Porter Dr., Palo Alto, C
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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CD613789.1 GI:40262053
                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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Exaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Homindae; Homo.

1 (bases 1 to 861)

Sota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y., and Isogai,T., RI human cDNA project (Ora,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y., Isogai,T.)

Londot: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 AGAATTGGAGCATGGAGCAAGAAGGATAATTGGAGGAAACCTGCTCCAGTGCATCTGC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 ACAGGCAACGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 507
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/db xref="taxon:9606"
/clone="PLACE400583"
/clone="Type="placenta"
/clone="Vector: pME18SFL3"
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                                                sapiens (human)
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       BST.
Homo sapiens
Homo sapiens
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Search completed: February 1, 2006, 12:22:51 Job time : 7324.56 secs

Title: Perfect score:

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Ad192189 Streptoki
Aaw1728 Streptoki
Aaw12891 Streptoki
Aaw12891 Streptoki
Aab01295 Wild type
Aab93425 Streptoki
Aar12282 Factor Xa
Aar12289 Streptoki
Aar12289 Streptoki
Aar12280 Streptoco
Aar2202 S.equisim
Aaw86144 Delmmuni
Aaw86144 Delmmuni
Aaw86144 Streptoco
Aay99593 Streptoco
Aay1725 Modified
Aay26020 Streptoki
Abb80012 Streptoki
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Abay4400 Mutant Et
Aaw21727 Streptoki
Aay84006 Amino aci
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Aar06378
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  -MODEL-frame+ n2p. model - DEV-x1p
-0-(cgn2_1/USPTO_bpool_p/US09940235/runat_27012006_144217_27548/app_query.fasta_1.7708
-0-(cgn2_1/USPTO_bpool_p/US09940235/runat_27012006_144217_27548/app_query.fasta_1.7708
-0-(cgn2_1/USPTO_bpool_p/US09940235/runat_27012006_144217_27548/app_query.fasta_1.7708
-0-(collide_bits_-CFMAFL=1 - END>-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-0-(collide_bits_-CFMAFL=1 - END>-1 - MATRIX=100 - THR_MIN=0 - ALIGN=15 - MODE-LOCAL
-0-(collide_bits_-CFMAFL=1 - END>-1 - THR_MAX=100 - THR_MIN=0 - ALIGN=15 - MODE-LOCAL
-0-(collide_bits_-CFMAFL=1 - END>-1 - THR_ANS=100 - THR_MIN=0 - MAXLEN=200000000
-0-(collide_bits_-CFMAFL=1 - END>-1 - MATRIX=0 - MAXLEN=200000000
-0-(collide_bits_-CFMAFR=1 - END>-1 - MATRIX=0 - MATRIX=0 - MAXLEN=0 - LONGLOG
-0-(collide_bits_-CFMAFR=1 - END>-1 - MATRIX=0 -
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Aar110194 Streptoki
Aar61120 Streptoki
Aay24794 Streptoco
Aaw94664 Streptoco
Aaw940585 Streptoco
Aay90185 Streptoco
Aay9185 Streptoco
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                                                                                                                                                                                                                                                                          tcgcttcacgttcgctcgcg......ataaccctaacgacaaataa 1782
                                                                                                                                            January 28, 2006, 01:47:34; Search time 123.96 Seconds (without alignments)
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                      protein search, using frame_plus_n2p model
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AAR121885
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AAY01556
AAY90282
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 2000000000
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   525 ArgProTyrLysGluLysProIleGlnAsnGlnAlaLysSerValAspValGluTyrThr 544
                                                                                                     TyrAspProPheAspArgSerHisLeuLysLeuDheThrIleLysTyrValAspValAsp
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/label= hirudin HV-1
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                                                             The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase; (3) an cucleic acid (1) encoding a modified bacterial streptokinase; (3) an cypression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a blood clots in patients with a thrombosic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of
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                                                                                                                                                                                                                                                                                                                                                                                             present sequence
                                                                                                                                                                                                                                                                                                                       plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates substrate site for protecolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence represents a streptokinase and maltose binding protein fusion protein from an example of the present invention
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N-terminally deleted streptokinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein is a recombinant product of a gene fusion construct. The sequence of the synthetic hirudin HV-1 genes was designed based on the published amino acid sequence (Dodt J., et al FEBS Letters 165 180 (1984)). The sequence of streptokinase was obtd. from PCR amplified chromosomal DNA from S. equisimilis ATCC 10009 or ATCC 9642. The primers used for the PCR were based on the pub- lished DNA sequence of S. equisimilis birrain H46A (Malke, H., Roe, B., and Perretti, J.J., Gene 34 357-362 [1985]). The two sequences were used to construct an expression vector in which the hirudin gene is linked to the streptokinase gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. Seals ARRI2887-R12889, ARRI2891-R12894 and AARI2522. (Updated on 25-WAR-
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                                                                                                                                                                                                                                                                                                                                          Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
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                                                          /label= streptokinase
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Pred. No.:
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                                                              Streptokinase and its derivatives can be produced in large quantities with high purity for use as thrombolytic agents in patients with lung thrombus or myocardial infarction. See also AAR10195-R10200
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DNA encoding a polypeptide which binds to plasminogen and corresponds to region of streptokinase - useful to detect plasminogen in a sample and to treat myocardial infarction.
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                                                                                                                                                                                             Streptokinase; SK; Streptococcus equisimilis; plasminogen; myocardial infarction.
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                                                                                                                                                                                                                                                         1. .352
/note= "claim 3, see
14. .414
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                                                                                                                                                                                                                                               Location/Qualifiers
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/note= "claim 3, £
244. .352
                                                                                                                                                                                                                           Streptococcus dysgalactiae subsp.
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120. .352
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244. .414
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                                                                                          AAR63120 standard; protein; 414
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16-NOV-1994
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29-SEP-1993;
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AspalaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAsp 360
                                                                                                                                         HISLEUALATYAN SPLYSAN SPARGTYT THREGING IN ART GEN VALLY SET TYLLEN 400
                                                       CATTTAGCCTATGATAAGATCGTTATACCGAAGAAGAAGAAGTTTACAGCTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes an isolated bacterial protein that
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                                                                                                                                                                                                                 Streptococcus equisimilis native streptokinase.
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              Length:
Matches:
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The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid The present sequence represents native SK. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPIg) to plasmin (HPIm), which is a serine protease able to catalyse the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus equisimilis H46A; streptokinase; mutant; fibrinoly plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; serine protesse; fibrin; blood clot; thrombolytic; serine protesse; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction;
                                                                                                                         Claim
                                                                                                                                                     Mutant streptokinase polypeptide - thrombolytic agent.
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hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K598 mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen (Updated on 17-OCT-2003 to standardise OS field)
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Conservative:

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US-09-940-235-11 (1-1782) x AAW94664
AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG
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The present sequence represents a native streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. P1 is used in thrombolytic
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This sequence represents the human Streptococcus equisimilus streptokinase protein sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, fibrin binding regions of human fibronectin, which are from fibrin binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a
                                                                                                                                                                                                                                                       Example 3; Fig 3; 58pp; English
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pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen to plasmin, thus adding in the localisation of the plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use Sequence 414 streptokinase. (Updated on 12-SEP-2003 to standardise OS field)

9.55e-193 2158.00 100.00% 100.00% 68.86%

Length:
Matches:
Conservative:
Mismatches:
Indels:

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ATTGCTGGACCTGAGTGGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCCAAGGCTTAAGTCCAAAAATCA SerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeuLysphePheGluIle AspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATC x AAY90282 (1-414)60 717 40 657 20

LysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPheGluVal AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACTACTTTGAGGTC LysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeu AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAAGCTGACTTACTA 120 897 100 837 80 777

LysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTTGCTAAGCGGACAT 1017 140 957

ValArgValArgProTyrLysGluLysProIleGlnAsnGlnAlaLysSerValAspVal GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG 160

GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA GluTyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGlyLeuLys 180 1077

200

TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG GCTCAAGCACAAAGCATTTTAAACAAAAAACCCACCCAGGCTATACGATTTATGAACGTGAC leTyrGluArgAsp

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N-PSDB; AAQ11651.
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  WPI; 1999-189643/16.
N-PSDB; AAX16633.
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Mutant streptokinase polypeptide - thrombolytic agent.
                                                          useful
                                                          a8
                                                          plasmin-resistant
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Claim 4; Col 11-14; 17pp;

The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the Pro88-Ly859-Ser60-Ly861 segment of the corresponding native SK is replaced by another amino acid The present sequence is mutant SK K59E. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPlg) to plasmin (HPlm), which is a serine protease able to catalyse the hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen

Sequence 414 AA;

Alignment Pred. No.:

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Percent Similarity:
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                                                                  AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
                                                                                              IleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAsp
                                                                                                      ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
                                                                                                                                 LysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeu
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GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 1077

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XX Harve
KW Pre-F
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XX Unide
XX WO200
XX WO1de
                                                                                                                                                                                                 24-MAY-2002; 2002EP-00077060.
07-FEB-2003; 2003US-00360101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  harvesting; recombinant; host cell; N-terminal leader peptide; pre-peptide; lantibiotic; post-translational modification; pharmaceuticals; vaccine; immunogenic.
Harvesting a desired polypeptide produced by a recombinant host cell,
                                                       WPI; 2004-042770/04.
                                                                                                                                                                                                                                                                     26-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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> producing pharmaceuticals, comprises selecting a recombinant nucleic comprising nucleic acid fragments encoding a leader peptide and the polypeptide. acid

Claim 4; Page 82-83; 109pp; English.

The invention relates to a novel method for harvesting a (poly)peptide produced by a recombinant host cell. The novel method involves selecting a cell comprising a first nucleic acid encoding a leader peptide and a second nucleic acid fragment encoding the desired (poly)peptide. The first and second fragments are within the same open reading frame of the first nucleic acid and the leader peptide is functionally equivalent to an N-terminal leader peptide found with the pre-peptide of a lantibiotic. The host cells and nucleic acids are useful for producing, harvesting and post-translational modification of polypeptides. The polypeptides may be used in the production of pharmaceuticals, e.g. as antigen for vaccine or immunogenic composition. This sequence represents a polypeptide relating to the novel method of the invention.

Sequence 413 AA,

2.8e-192 2153.00 100.00% 100.00% 68.70%

Length: Matches: Conservative: Mismatches: Indels: Gaps:

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GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 1137 		SATATATATATATATATATATATATATATATATATATAT	GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTTGATGTT 1017	LysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis 140				LysālaIleGlnGluGlnLeuIleālaāsnValHisSerāsnāspāspTyrPheGluVal 100		. LysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeu 80		AspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer 60		SerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeuLysPhePheGluIle 40		. IleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal 20		-11 (1-1782) x ADL92189 (1-413)

1138 GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 1197

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Protein
           09-JUN-1995;
                                   07-JUN-1996;
                                                                                                                       Protein
                                                                                                                                                                                                                    Plasminogen-binding thrombolytic agent;
                                                                                                                                                                                                                                                         Streptokinase/maltose binding
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01-OCT-1997
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                                                                                                                                                                                                                                                                                                                                               standard;
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           95US-00488940
                                   96WO-US009640
                                                                                                         /label= Maltose_binding_protein
/note= "acts as blocking group"
382. .1194
/label= Streptokinase
                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              protein; 1194
                                                                                                                                                                                                                    fragment; streptokinase; degradation; MBP; blood clot; bolus; maltose-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a fusion protein between maltose-binding protein and the plasminogen-binding fragment of streptokinase. This fusion protein was used in the design of modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, optionally as a bolus rather than by continuous infusion. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 11-12; 65pp; English.
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                                                                   AGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTGGAATATACT
                                                                                                       SerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHisValArgVal
                                                                                                                                                   AlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAspLysAspGly
                                                                                                                                                                                                    GlnGlnGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPheGluValIleAspPhe
                                                                                                                                                                                                                  CAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTCATTGATTTT
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                                                                                                                               TCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTTGCTAAGCGGACATGTGCGCGTT
                                                                                                                                                                                                                                                       AlaThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeuLysAlaIle
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966 504 906 484 846 464 786 444 726 424 666 404 606 384

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17-SEP-1991
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                                                                  Protein
                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
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(first entry)
                                                                                                                                                                                             dysgalactiae subsp. equisimilis;
                                                                                                                                                                                                                                        blood clotting; coagulation; thrombolysis; streptokinase.
                                                                                  /label= pre-pro alpha factor
/note= "S. cerevisiae"
                                           /label= mature streptokinase
                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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                                                                                                                                                                                                                                                                 fibrinolysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The streptokinase sequence was obtd. from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C) ATCC 10009 or ATCC 9642 (the primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]). The gene was fused to DNA encoding the yeast alpha factor pre-pro-secretion sequence in an expression vector, pSMD1/152, for prodn. of recombinant strepto- kinase in S. cerevisiae strain BJ2168. See also AAR12887-R12889, AAR12892-R12894, AAR12885 and AAR12522. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pusion protein cleavage by blood clotting enzyme - fractions having greater antithrombotic activity for prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 499
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07-DEC-1990;
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                                                 GlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPheGluValIleAspPhe
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                                                                                                GlyThrValGluGlyThrAsnGlnAspIleSerLeuLysPhePheGluIleAspLeuThr
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               Plasminogen-binding fragment; streptokinase; degradation; MBP; thrombolytic agent; blood clot; bolus; maltose-binding protein
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as thrombolytic
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ValargValarg---TyrLysGluLysProIleGlnAsnGlnAlaLysSerValAspVal 159
                                                                                               ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
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                                                  LysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             forms of streptokinase resistant to enzymatic cleavage - useful bolytic agents in treating thrombosis and in medical equipment.
                                                                                                                                                                                                                                                                                                                                               IleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal
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                               dysgalactiae
                                                                 (SK)
                                             therapeutic; streptokinase.
                                                   epitope; T-cell; immunogenicity;
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21-MAY-1997;
31-JUL-1997;
28-NOV-1997;
02-DEC-1997;
14-APR-1998;
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                                                                                                     (BIOV-) BIOVATION LTD
                                                                                                             97GB-00010480.
97GB-00016197.
97GB-00025270.
97US-0067235P.
98GB-00007751.
                                                                                                                                     98WO-GB001473
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Reducing immunoc sequence of the given species. immunogenicity of proteins - by modifying the amino acid of the protein to eliminate potential epitopes for T-cells 0f B

6; Fig 28; 77pp; English.

The invention relates to a method for the production of non-immunogenic CC proteins. The method comprises determining at least part of the amino CC acid sequence of the protein; (b) identifying in the amino acid sequence on or more potential epitopes for T-cells (T-cell epitopes) of the given CC species; and (c) modifying the amino acid sequence to eliminate at least CC one of the T-cell epitopes identified in step (b) thereby to eliminate or CC reduce the immunogenicity of the protein when exposed to the immune CC system of the given species. A method of analysing a pre-existing protein CC to predict the basis for immunogenic responses is also provided. The CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The CC compresents the amino acid sequence of the SK protein. (Updated on 17-OCT-CC 2003 to standardise OS field)

Seguence 414 Ā

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                  Score:
US-09-940-235-11 (1-1782) x AAW86143 (1-414)
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                  2.6e-190
2132.00
99.03%
98.79%
68.03%
                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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1738 CGTTATACAGGGACACCTATACCTGATAACCCTAACGACAAA 1779 	1678 CATTTAGCCTATGATAAAGATCGTTATACCGAAGAAGAACGAGAAGTTTACAGCTACCTG 1737 	1618 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGCTA	1558 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 161 	1498 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 155	1438 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1497	1378 GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 143 	N H	N H	1198 TCCTCAATGGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 125	1138 GCTCAAGCACAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 119	1078 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 113	1018 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 107 	958 GTGCGCGTTAGACCATATAAAGAAAAACCAATACCAAAACCAAGCGAAATCTGTTGATGTG 101 	121 LysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis 140
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Search completed: January 28, 2006, 02:08:39 Job time: 145.96 secs

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2: /cgn2_6/ptodata/]

3: /cgn2_6/ptodata/]

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Patent No. 5240845
Sequence 52, Appl
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e 2, Appl	nce 4,	ent No. 545515	equence 1, Appl	equence 12,	equence 235, Ap	e 16,	equence 2,	equence 2,	Sequence 1, Appli	equence 1,	e 14,	e 12, Āpp	4.	, App	40,	3, Appl	Φ ω,	0.4	e 4,	e 2, App	ν	equence	equence 1,	equence 2,	4	equence 12,	Sequence 12, Appl	equence 12,	equence 18,	e 17,	equence 35, Ap	Sequence 47, Appl

## ALIGNMENTS

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Sequence 2, Application US/09211542A
Patent No. 6210667
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWBERG & SUNSTEIN, LLP
STREET: 125 Summer Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFEICATION INFORMATION:
APPLICATION NUMBER: 06/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: Atcorney, Strimpel, Harriet M.
REGISTRATION UMMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELEPHONE: (617)443-9292
TELEPAX: (617)443-9004
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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RESULT 2
US-07-854-596B-43
                                                APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 43-596B
ATTORNEY/AGENT INFORMATION:
NAME: MCDOTHEll, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
TELEPAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-Lease #1.0, V
CURRENT APPLICATION DATA:
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APPLICANT: Hunter, Michael G
APPLICANT: Czapłewski, Lloyd G
TITLE OF INVENTION: Proteins and
TOPOLOGY: 1: MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
                                  TYPE: amino acid
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Best Local Similarity:
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US-09-211-542A-6
(S-09-211-542A-6)
; Sequence 6, Application US/09211542A
; Patent No. 6210667
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIPICATION: 1653
PRIOR APPLICATION DATA:
APPLICA
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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STREET: 12
CITY: Bost
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REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)443-9292
TELEPAX: (617)443-9292
TELEFAX: (617)443-9292
TELEFAX: (617)443-0004
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TYPE: protein
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/I
FILING DATE: 06-JUL-1990
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RESULT 4
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;Patent No. 5240845
; APPLICANT: PUJII, SETSURO;TAKADA, KAORUKO;. KATANO, TAMIKI;
MAJIMA, EIJI;OGINO, KOICHI;ONO, KENJI;SAKATA, YASUYO;UENOYAMA,
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GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGGCAAGGCTTAAGTCCAAAATCA 717
                                                AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC 657
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                                   HisLeuAlaTyrAspLysAspArgTyrThrGluGluGluArgGluValTyrSerTyrLeu
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CORRESSEE: Evenson, McKeown, Edwards & Lenana STREET: 1200 G Street, N.W., Suite 700 CITY: Washington CITY: Washington STATE: DC COUNTRY: USA ZIP: 20005

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER FIOR SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1. CURRENT APPLICATION UNMBER: US/08/560,098A FILING DATE: 17-NOV-1995

PRIOR APPLICATION UNMBER: US/08/560,098A FILING DATE: 17-NOV-1994
APPLICATION NUMBER: US/08/560,098A FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION: NAME: EVANS, JOSEPh D. REGISTRATION UNMBER: 26,269
REFERENCE/DOCKET NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 18/42448
TELECOMMUNICATION: INFORMATION: TELEPAN: (202) 628-8800
TELEPAN: (202) 628-8800
TELEPAN: (202) 628-8801
TELEPAN: (202) 628-801
INFORMATION FOR SEQ ID NO: 52: SEQUENCE CHARACTERISTICS: I-ENGTH: 440 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 440 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-560-098A-52
                                                                                                                                                                                                                                                                                                                                                                                                           US-09-940-235-11 (1-1782) x US-08-560-098A-52 (1-440)
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APPLICANT: WIENUT, Stephan

APPLICANT: HEINZEL-WIELAND, Regina

APPLICANT: STEFFENS, Gerd Josef

TITLE OF INVENTION: Proteins having Fibrinolytic

TITLE OF INVENTION: Coagulation-inhibiting Proper

NUMBER OF SEQUENCES: 60
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AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAAGCTGACTTACTA
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Suite 700
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RESULT 6
US-10-360-101-264
Sequence 264, Application US/10360101
Patent No. 6861236
GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of
PILE REFERENCE: 2183-5673
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CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: ED 2077060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: PatentIn version 3.1
SEQ ID NO 264
LENGTH: 413
TYPE: PRT
ORGANISM: Artificial Sequence
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                GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
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Patent No. 5854049
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOTTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,940

FILING DATE: 09-JUN-1995

CLASSIFICATION: 514
                            TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PI
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Guy
                                                                                                                                                                                                                                           STREET: 225 F
CITY: Boston
STATE: MA
COUNTRY: USA
TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
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RESULT 8
US-07-854-596B-28
US-07-854-596B-28
; Sequence 28, Applic;
; Patent No. 5434073
; Patent No. 5434073
  Pred. No.:
Score:
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                           Alignment Scores:
                                                    ; MOLECULE TYPE:
US-07-854-596B-28
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APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
                                                                                                                           TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                            REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION MAMBER: US/07/854,596B
FILING DATE: 03-UN-1992
                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                         STATE: I
                                                                                                                                                      TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
                                                                            TYPE: amino acid TOPOLOGY: linear
                                                                                                  LENGTH: 499 amino acids
                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dr. John J. McDonnell STREET: Ten South Wacker Drive,
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                                                                             linear
                                                                protein
  1.42e-208
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  Length:
Matches:
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Query Match:
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ACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAACTTTAGACTTC 1506
                                    ATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGGGAAAAGCCG 1380
                                                                                                                                         HisValLysAsnArgGluGlnAlaTyrGluIleAsnLysLysSerGlyLeuAsnGluGlu
                                                                                                                                                                                                        GlnSerIleLeuAsnLysThrHisProGlyTyrThrIleTyrGluArgAspSerSerIle
                                                                                                                                                                                                                                                         CAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGACTCCTCAATC 1206
                                                                                                                                                                                                                                                                                              LeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAla
                                                                                                                                                                                                                                                                                                          CTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTAGCTCAAGCA 1146
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                                                                                        IleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLysGlyGluLysPro
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95.82%
68.38%
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1	08-488-940-3 (1-813)	68.30% Indels:	Pred. No.: 3.26e-208 Length: 813 Score: 2140.50 Matches: 413 Percent Similarity: 99.76% Conservative: 0 Best 10031 Similarity: 90.76% Minmatches: 0	Scores:	MOLECULE TYPE S-08-488-940-3	TYPE: amino acid STRANDEDNESS: not TOPOLOGY: linear	INFORMATION FOR SEQUENCE CHARAC	TELEFAX:	; REGISTEATION NUMBER: 34,819 ; REFERENCE/DOCKET NUMBER: 05433/009001 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 617/542-5070			OPERATING SYSTEM: PO SOFTWARE: Patentin F CURRENT APPLICATION DAT				CORRESPONDENCE ADDRESS ADDRESSEE: Fish & R	; TITLE OF SECUENCES: 20	Sequence 3, Application ( Patent No. 5854049 GENERAL INFORMATION:	ESULT 9 S-08-488-940-3		Qy 1747 GGGACACCTATACCTGATAACCCTAACGACAAA 1779		₽	Cy 1627 ATCATAACCGTTTATATGGGCAAGGAGGAGAAATGCTAGCTA	429 G	1567 GGTAT	409 ArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPhe	1507 AGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTT	Db 389 ThrAsnGluLeuLeuLvsSerGluGlnLeuLeuThrAlaSerGluArgAsnLeuAsnPhe 408
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1618 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAGA	340 AspAlaPheGlylleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAsp 359	1558 GATGCTTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1617	1498 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 1557	AspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsn	1438 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1497	1370 GAMANGCUSIAIGHICCIIIIGHICGCAGIGHCIIGHAMACIGIICACCAICANAIAUGII 1437 	AsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLysGly	1318 AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAAGGG 1377	1258 TITACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 1317 			1138 GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 1197 	180 AspThrLysLeuLeuLysThrLeuAlaileGlyAspThrIleThrSerGlnGluLeuLeu 199	1078 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 1137	1018 GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 1077 	ValArgValArgTyrLysGluLysProlleGlnAsnGlnAlaLysSerValAspVal	958 GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAAACCAAGCGAAATCTGTTGATGTG 1017	898 AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCCAAGAATTTTTGCTAAGCGGACAT 957	01 IleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAsp	838 ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC 897		AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC 8		41 AspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer 60 718 AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA 777	658 GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGAGCAAGGCTTAAGTCCAAAATCA 717	21 SerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeuLygPhePheGluIle 40	AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC	1	л

Oy  Oy  S18 ATTGCTGGACCTGAGTGGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT  Db  2 IIEAlaGlyProGluTTpLeuLeuAspArgProSerValAsnAsnAsnSerGlnLeuValVal  Oy  S18 AGCGTTGCTGGTACTGTTGAGGGGGACGAATTGGTTGTT  Oy  S18 AGCGTTGCTGGTACTGTTGAGGGGGACGAATCAAGACAGCCAATTGGTTGTT  Oy  S19 AGCGTTGCTGGTACTGTTGAGGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC  Oy  658 GATCTAACATCACGACCTGCTCATGAGAGAAAGACAGGCTTAAGTCCAAAATCA  OY  658 GATCTAACATCACGACCTGCTCATGAGGAAAAGACAGAGCAAAGGCTTAAGTCCAAAATCA  ON  ON  ON  ON  ON  ON  ON  ON  ON  O	d. No.: 1.69e-207 Length: re: 2132.00 Matches Cent Similarity: 99.03% Conserv Local Similarity: 98.79% Mismatc Fy Match: 68.03% Indels: 1 Gaps:	NCE CHARACTERISTICS: GTH: 415 amino acid E: amino acid OLOGY: linear ULE TYPE: protein 596B-26 Scores:	UNICATION INFORMATION: ONE: 312-715-1000 K: 312-715-1234 910-221-5317 910-221-5317 N FOR SEQ ID NO: 26:	APPLICATION NUMBER: US/07/854,596B FILING DATE: 03-JUN-1992 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: McDonnell, John J REGISTRATION NUMBER: 26,949 REGISTRATION NUMBER: 26,949 REGISTRATION NUMBER: 26,949		; AFFLICANI: CZEDLEWSKI, LIDYG G ; TITLE OF INVENTION: Proteins and nucleic acids ; NUMBER OF SEQUENCES: 73 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Dr. John J. McDonnell ; STREET: Ten South Wacker Drive, Suite 3000 ; CITY: Chicago ; STATE: IL	26 Application US/07854 34073 RMATION: Dawson, Keith M Hunter, Michael G	Qy 1738 CGTTATACAGGGACACCTATACCTGATAACCCTAACGACAAA 1779 	1678 CATTTAGCCTATGATAAAGATCGTTATACCGAAGAAGAAGAAGAGAGAG	Db 360 Thragapart 10110Thragal Turker 1777 and 20120111111111111111111111111111111111
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ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCGAAGGAGAATGCTAGCTA	1498 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 1557		AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG	1198 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 1257	1078 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTAGAATTACTA 1137	958 GIUGGCGTTAGACCATATAAGAAAACCATACAAACCAGAGAATCTGTTGATGTG 1017		778 AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC 837	718 AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA 777 	42 AspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer 61

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER IBM PC COMPATIBLE
COMPUTER IBM PC COMPATIBLE
COMPUTER IBM PC COMPATIBLE
COMPUTER IBM PC COMPATIBLE
COMPUTER: O3-JUN-1992
CILASSIFICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CILASSIFICATION INFORMATION:
NAME: MCDONNell John J
REGISTRATION NUMBER: 92,337
REGISTRATION NUMBER: 92,337
REFERENCE/DOCKET NUMBER: 92,337
REJECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1234
TELEPHONE: 312-715-1234
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TELEPAX: 312-715-1234
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TELEPAX: 435 amino acids
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US-07-854-596B-19
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GENERAL INFORMATION:
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 73
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TYPE: amino acid
TOPOLOGY: linear
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            AspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSer
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Sequence 15, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
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Percent Similarity:
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Query Match:
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STREET: Ten Sout
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE E
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APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UUV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92
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E: Dr. John J. McDonnell
Ten South Wacker Drive, Suite 3000
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                                                                                                                    GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 73
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive,
                                                    CITY:
STATE:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UNN-1992
CLASSIFICATION: 435
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                                                                                                                                     AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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                                       GluTyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGlyLeuLys
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Matches:
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ArgTyrThrGlyThrProIleProAspAsnProAsnAspLys
                       CGTTATACAGGGACACCTATACCTGATAACCCTAACGACAAA 1779
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US-07-854-96B-35
Sequence 35, Application US/07854596B
Patent No. 5434073
Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Bowson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
CCRRESPONDENCE ADDRESS:
ADDRESSEE Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER : IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-7UN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDORNEY: 26,949
REGISTRATION NUMBER: 26,949

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Percent Similarity:
Best Local Similarity:
Query Match:
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TELEPHONE: 312-715-1000
TELEPHAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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TYPE: amino acid
TOPOLOGY: linear
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TTTACTTACAGTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG
                                                                                                                                  GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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                                              SerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu
                                                                    TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
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      IleaspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAsp

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Matches:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino
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Patent No. 5854049
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
                                                                                                                                              APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/0090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
   MOLECULE TYPE:
                                                                                                                              TELEPHONE: 617/542-50
TELEFAX: 617/542-8906
                  STRANDEDNESS: not relevant TOPOLOGY: linear
                                                 TYPE: amino acid
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                                                                      AGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTGGAATATATACT
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TATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTTGATGTCGAT 1446
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96.52%
96.29%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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79 4	GTTTACAGCTACCTGCGTTATACA 1746 	GAGAATGCTAGCTATCATTTAGCC 1686	GATAATCACGATGACACCAACCGT 1626 	CTCTACAACAATCTCGATGCTTTT 1566 	GCTAGCGAACGTAACTTAGACTTC 1506 	

Search completed: January 28, Job time : 48.4212 secs 2006, 02:41:40

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Perfect score:
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1: /cgn2_6/ptodata/1/pubpaa/US07
2: /cgn2_6/ptodata/1/pubpaa/US09
3: /cgn2_6/ptodata/1/pubpaa/US09
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6: /cgn2_6/ptodata/1/pubpaa/US11_
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Match
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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US-10-988-943-1

US-10-909-703-12

US-10-474-792-658

US-10-236-392-2

US-10-236-392-2

US-10-236-392-9

US-10-236-392-9
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Sequence 2, Appli
Sequence 254, App
Sequence 252, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 273, App
Sequence 658, Appli
Sequence 658, Appli
Sequence 670, Appli
Sequence 98, Appl
Sequence 98, Appl
Sequence 98, Appl
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-10-741-600-1	-10-618-281-3	-10-788-792-20	US-10-741-601-360	-09-961-403-	-040-130-2	US-10-287-436A-1137	-10-287-436A-	852	-10-741-600-1	-10-741-600-	-10-491	US-10-741-601-366	-10-741-601-	-10-734-564-	-10-447-161-	$\sim$	-10-144-	-10-279-733-	-10-741-600-	-10-741-601-	-236-392-	-741-600-	-10-741-6	-10-741-600-	-10-741-60	-10-741-600-10	-10-741-	1-566-	-10-144-194A	-10-477-173-6	0	US-10-477-238A-677
107	32,	206	36	Sequence 1, Appli	28	111	Sequence 436, App	14.	1078,	10	e 10.	e 36	Sequence 357, App	94	Sequence 3, Appli	23	í	8	10	8	Sequence 4, Appli	100	e 356,	e 1072	e 359,	1066	354,	52	equence 52,	equence	equence 677,	Sequence 677, App

## ALIGNMENTS

Percent Similarity: Best Local Similarity: Score: ; TYPE: PRT ; ORGANISM: Streptococcus equisimilis US-09-940-235-2 RESULT 1 US-09-940-235-2 Pred. No.: Alignment Scores: CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 4 GENERAL Sequence 2, Application US/0940235 Publication No. US20030059921A1 APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN APPLICANT: Kumar, Rajesh APPLICANT: Sahni, Girish APPLICANT: Roy, Chait INFORMATION: 414 Girish 3.4e-192 2158.00 100.00% 100.00% Length:
Matches:
Conservative:
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PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 264
LENGTH: 413
TYPE: PRI
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification
FILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
                                                                                                                                                                                                                                                                                    FEATURE:
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RESULT 3
US-10-300-215-252
; Sequence 252, Application US/10300215
; Publication No. US20030153043A1
; GENERAL INFORMATION:
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APPLICANT: CARR, Francis Joseph
APPLICANT: ADAIR, Fiona Suzanne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: CARTER, Graham
TITLE OF INVENTION: MCTHOD FOR THE PRODUCTION
TITLE OF INVENTION: MON-IMMUNOGENIC PROTEINS
FILE REFERENCE: MER-104-Con.1
CURRENT APPLICATION NUMBER: US/10/300,215
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PRIOR APPLICATION NUMBER: US 09/438,136
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: GB 9710480.6
PRIOR FILING DATE: 1997-05-21
PRIOR REPLICATION NUMBER: GB 9716197.0
PRIOR PILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-11-28
PRIOR PILING DATE: 1997-11-28
PRIOR APPLICATION NUMBER: GB 9807751.4
PRIOR APPLICATION NUMBER: GB 9807751.4
PRIOR APPLICATION NUMBER: US 60/067,235
PRIOR PILING DATE: 1997-11-02
PRIOR APPLICATION NUMBER: US 60/067,235
PRIOR PILING DATE: 1997-12-02
NUMBER: OF SEO ID NOS: 254
SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 252
LENGTH: 414
TYPE: PRT
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US-10-988-943-1
US-10-988-943-1
; Sequence 1, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
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                                                                                                                     APPLICANT: Center for Genetic Engineering and Biotechnology
TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR
TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS
TITLE OF INVENTION: COMPLEX MIXTURES.
FILE REFERENCE: PROTeomics CU2003-269
CURRENT APPLICATION NUMBER: US/10/988,943
CURRENT FILING DATE: 2004-11-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
                                                                                     LENGTH: 415
TYPE: PRT
ORGANISM: Streptococcus
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                                                TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
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Sequence 253, Application US/10300215
Publication No. US20030153043A1
GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
APPLICANT: ADAIR, Fiona Suzanne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: HAMILTON, METHOD FOR THE PRODUCTION OF
TITLE OF INVENTION: MCHOD FOR THE PRODUCTION OF
TITLE OF INVENTION NUMBER: US/10/300,215
CURRENT FILLING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 09/438,136
PRIOR APPLICATION NUMBER: WD PCT/GB98/01473
PRIOR APPLICATION NUMBER: GB 9716197.0
PRIOR APPLICATION NUMBER: GB 9716197.0
PRIOR APPLICATION NUMBER: GB 9716197.0
PRIOR APPLICATION NUMBER: GB 9725270.4
PRIOR APPLICATION NUMBER: GB 9807751.4
PRIOR APPLICATION NUMBER: US 60/067,235
PRIOR APPLICATION NUMBER: US 60/067,235
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/067,235
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 254
SOFTMARE: PASTSEQ for Windows Version 4.0
SOFTMARE: PASTSEQ for Windows Version 4.0
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Pred. No.:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Krystal, Gerald

APPLICANT: Rabkin, Simon W.

TITLE OF INVENTION: Peptides and Their Use to Ameliorate

TITLE OF INVENTION: Cell Death

FILE REFERENCE: 50216/00304

CURRENT APPLICATION NUMBER: US/09/919,703

CURRENT FILING DATE: 1090-04-19

PRIOR APPLICATION NUMBER: US 09/294,457

PRIOR APPLICATION NUMBER: US 09/294,599

PRIOR APPLICATION NUMBER: US 08/759,599

PRIOR APPLICATION NUMBER: US 60/008,233

PRIOR PILING DATE: 1995-12-06

NUMBER OF SEQ ID NOS: 16

SOPTWARE: FRASTSEQ for Windows Version 4.0

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TYPE: PRT
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 GATACTAAGCTATTGAAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 1137
                                                                   ValArgValArgProTyrLysGluLysProTleGlnAsnGlnAlaLysSerValAspVal
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Percent Similarity:
Best Local Similarity:
                        Score:
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                                                                     ; ORGANISM: Streptococcus pyogenes US-10-474-792-658
                                                                                           LENGTH: 440
TYPE: PRT
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Sequence 658, Application US/10474792

Publication No. US20040236072A1

GENERAL INFORMATION:
APPLICANT: Olmsted, Stephen
APPLICANT: Cagursky, Robert
APPLICANT: Winter, Lourie
APPLICANT: Winter, Lourie
TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
SEQ ID NO 658
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FILE REPERENCE: 21402-442A
CURRENT APPLICATION NUMBER: US/10/236,392
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US/9/540,763
PRIOR APPLICATION NUMBER: US/9/59,155
PRIOR APPLICATION NUMBER: US/9/635,949
PRIOR APPLICATION NUMBER: US/9/635,949
PRIOR PILING DATE: 2000-08-10
PRIOR PILING DATE: 2000-08-10
PRIOR PILING DATE: 2001-09-12
PRIOR PILING DATE: 2001-09-12
PRIOR PILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/9/357,303
PRIOR PILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US/9/367,753
PRIOR PILING DATE: 2002-03-25
PRIOR PILING DATE: 2002-04-02
PRIOR PILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: US/9/659,634
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APPLICANT:
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APPLICANT: Smithson, Glennda
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES,
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Shenoy, Suresh
Shimkere
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Grosse, William M
Gusev, Vladamir
Kekuda, Ramesh
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Catterton, Blina
Chapoval, Andrei
Crabtree, Julie
Bdinger, Shlomit, F
Ellerman, Karen
Gerlach, Valerie
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Rastelli, Luca
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Pena, Carol A
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Malyankar, Uriel
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RESULT 9
US-10-171-311-64
; Sequence 64, Application US/10171311
; Publication No. US20030087270A1
; Publication No. US20030087270A1
; Publication No. US20030087270A1
; Publicant: Chen, Yan
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Glatt, Mariula
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; LENGTH: 2320
; TYPE: PRT
; ORGANISM: Homo s
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PRIOR FILING DATE: 2001-09-07
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 794
SOFTWARE: Custom
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Percent Similarity:
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Query Match:
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
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GluProCysValLeuProPheThrTyrAsnGlyArgThr 343
                                             CGACCT------GCTCATGGAGGAAAGACA 693
                                                                                                                                        ACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATCGATCTAACATCA
                                                                                                                                                                                   GlnTrpLeu-----LysThrGlnGlyAsnLysGlnMetLeuCysThrCysLeuGly
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APPLICANT: Gullans, Steven R.
APPLICANT: Bueno, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic Tests
FILE REFERENCE: B00801/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236,031B
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/317,389
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.1
SEQ ID NO 700
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APPLICANT: Jensen, Roderic
APPLICANT: Gullans, Steven
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| GluProCysValLeuProPheThrTyrAsnGlyArgThr 343
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                                                                                                            ACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATCGATCTAACATCA
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                                                                        AsnGlyValSerCysGlnGluThrAlaValThrGlnThrTyrGlyGlyAsnLeuAsnGly
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                                      -GCTCATGGAGGAAAGACA 693
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CURRENT FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: US 09/544,398
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 09/543,771
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1999-01-13
PRIOR APPLICATION NUMBER: US 60/071,449
PRIOR APPLICATION NUMBER: US 60/071,449
PRIOR APPLICATION NUMBER: US 60/105,511
PRIOR PILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 109
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; ORGANISM: Homo
US-10-374-979-98
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US-10-374-979-98
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TITLE OF INVENTION: THE HIGH BONE MASS GENE
FILE REFERENCE: 032796-021
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AsnGlyValSerCysGlnGluThrAlaValThrGlnThrTyrGlyGlyAsnLeuAsnGly
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                                                                                                          GAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTTAGCGTTGCTGGT 609
                                                                                                                                              GlnProProTyrGlyHisCysValThrAspSerGlyValValTyrSerValGlyMet
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                                    ACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATCGATCTAACATCA
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No. US20030219793A1
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; ORGANISM: Homo
US-10-182-936A-98
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US-10-182-936A-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/291,311
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: US 60/361,293
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 216
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APPLICANT: Yaworsky, Paul
TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions
FILE REFERENCE: 032796-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US02/15982
PRIOR FILING DATE: 2002-05-17
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              GlnProProTyrGlyHisCysValThrAspSerGlyValValTyrSerValGlyMet
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                                                                    SerGlySerGlyProPheThrAspValArgAlaAlaValTyrGlnProGlnProHisPro
                                                                                        ACAGGCAACGGCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG
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; TYPE: PRT
; ORGANISM: Homo s
US-10-477-238A-677
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APPLICANT: Yawore
APPLICANT: Bex, I
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             508 AGCGGATCTGGCCCCTTCACCGATGTTCGTATTGCT
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FILE REFERENCE: 032796-212
CURRENT APPLICATION NUMBER: US/10/477,238A
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: US 60/290,071
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR PLICATION NUMBER: US 60/291,311
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: US 60/361,293
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 812
SOFTWARE: FASESEQ for Windows Version 4.0
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APPLICANT: Bex, Frederick J. III
APPLICANT: Bodine, Peter Van Nest
TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT
                                                                                                                                                                                                                                                             194 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr
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                                      ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer
                                                                                                    ACAGGCAACGGCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG
                                                                                                                                                   ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysIleCys
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o. US20040221326A1
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Matches:
Conservative:
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Query Match:
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US-10-680-287A-677
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US-10-680-287A-677
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GENERAL INFORMATION:
APPLICANT: Babij, ph
APPLICANT: Yaworsky
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CURRENT FILING DATE: 2003-10-08
PRIOR APPLICATION NUMBER: PCT/US02/14876
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/290,071
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/291,311
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR APPLICATION NUMBER: US 60/361,293
PRIOR APPLICATION NUMBER: US 60/361,293
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SEQ ID NO 677
LENGTH: 2328
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APPLICANT: Bodine, Peter Van Nest
TITLE OF INVENTION: Transgenic Animal Model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 812
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|GlnTrpLeu-----LysThrGlnGlyAsnLysGlnMetLeuCysThrCysLeuGly 310
AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                     GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr
                                                                                           GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT
                                                                                                                           TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer
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Best Local Similarity:
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US-10-477-173-677
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PRIOR APPLICATION NUMBER: US/10/477,173
PRIOR APPLICATION NUMBER: US 60/290,071
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/291,311
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR APPLICATION NUMBER: US 60/351,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 677, Application US/10477173 
Publication No. US20050070699A1 
GENERAL INFORMATION:
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SEQ ID NO 677
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APPLICANT:
APPLICANT:
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APPLICANT: Allen, Kristina M.
APPLICANT: Yaworsky, Paul
APPLICANT: Morales, Arturo J.
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NUMBER OF SEQ ID NOS: 1086
SOFTWARE: FastSEQ for Windows Version
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TITLE OF INVENTION: HBM Variants that Modulate
FILE REFERENCE: 032796-135
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                                 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGGACTTCCTATGTGGTCGGAGAAACG 313
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and Lipid Levels

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670 331	610 311	550 294	544 274	508 254	448 234	388 214	328 194	174
CGACCTGCTCATGGAGGAAAGACA 693          :::      :::    GluProCysValLeuProPheThrTyrAsnGlyArgThr 343	ACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATCGATCTAACATCA 669 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::	GAGTGGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTTAGCGTTGCTGGT 609 :::       GlnTrpLeuLysThrGlnGlyAsnLysGlnMetLeuCysThrCysLeuGly 310	GlnProProTyrGlyHisCysValThrAspSerGlyValValTyrSerValGlyMet 293	AGCGGATCTGGCCCCTTCACCGATGTTCGTATTGCT	ACAGGCAACGGCCGAGGAGAGTGGAAAGTGTGAGAGGGCACACCTCTGTGGAGAGACCACATCG 507	AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC 447 	328 GGACGCATCACTTCCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT 387 	     TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 193

Search completed: January 28, 2006, 02:57:14 Job time : 140.535 secs

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Result
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-Q=/cgn2 1/USPTO_spool_p/US09940235/runat_27012006_144220_27676/app_query.fasta_1.7708
-Q=/cgn2 1/USPTO_spool_p/US09940235/runat_27012006_144220_27676/app_query.fasta_1.7708
-DB=Published_Applications_AA New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1
-LOOPEX=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -QUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US09940235_@CGN 1 1 @runat 27012006_144220_27676
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBIOCX=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB
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Perfect score:
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Maximum Match 10
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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  US-10-631-558-2

US-11-032-951-12

US-10-995-561-621

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US-10-995-561-627

US-10-995-561-626

US-10-995-561-626
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Sequence 2, Appli
Sequence 12, Appl
Sequence 631, App
Sequence 622, App
Sequence 623, App
Sequence 633, App
Sequence 637, App
Sequence 627, App
Sequence 1545, Ap
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130	Sequence 126, App	128	20,	33,	106	33	32,	31,	Sequence 11, Appl	108,	10	82,	e 171,	e 292,	e 29,	e 141,	e 14(	96	7,	e 31:	æ	63	e 8	e 7	e 4	e 13	e ა	e 62,	equence 62:	equence 630	equence 625	equence 632, Ap	e 4	Sequence 31, Appl

## ALIGNMENTS

US-10-631-558-2

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Publication No. US20050260598A1
GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Roy, Chait
APPLICANT: Roy, Chait
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
FILLE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR PILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 1N 3825/DEL/98
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 414
TYPE: PRT
ORGANISM: Streptococcus equisimilis
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Alignment Scores:

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GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
                                                                                                                                                                       GlulysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal
                                   GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                    GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
                                                                                                                                                                                                                                       GTGGGGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
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                                                                                                                      TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
                                                                                                                                           GluTyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGlyLeuLys
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Percent Similarity:
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Query Match:
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APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Peptides and Their Use t
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/003005
CURRENT APPLICATION NUMBER: US/11/032,951
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: US 09/919,703
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
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US-11-032-951-12
                                                                                                                                                                                           US-09-940-235-11 (1-1782) x US-11-032-951-12 (1-413)
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SOFTWARE: FastSEQ for Windows
SEQ ID
12
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                         ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACACAGCCAATTGGTTGTT
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RESULT 3
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|LeuArgTyrThrGlyThrProIleProAspAsnProAspAspLys
                                                                                         TATCATTTAGCCTATGATAAAGATCGTTATACCGAAGAAGAAGGAGGAGGTTTACAGCTAC 1734
                                                                                                                                              AACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAAT
                                                                                                                                                                                                                                                                                                                  GTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGT
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRU
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
                                                                                                                    Sequence 622, Appublication No.
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; Sequence 631, Application US/1099561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
i APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WIT
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
; CURRENT PILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 631
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Homo sapiens
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                                                                          321 GlnTrpLeu-----LysThrGlnGlyAsnLysGlnMetLeuCysThrCysLeuGly
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|TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer
Application US/10995561
o. US20050272054A1
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US-10-995-561-629
Sequence 629, Application US/10995561
Publication No. US20050272054A1
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Best Local Similarity:
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                                                                SEQ ID NO 629
LENGTH: 984
TYPE: PRT
ORGANISM: Homo s
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SEQ ID NO 622
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo say
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 633, Application US/1099561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPON
TITLE OF INVENTION: DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 633
LENGTH: 2296
                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-995-561-633
                                                                                                       US-09-940-235-11 (1-1782) x US-10-995-561-633 (1-2296)
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321 GlnTrpLeu-----LysThrGlnGlyAsnLysGlnMetLeuCysThrCysLeuGly
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US-10-995-561-623
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Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
                                                                                                                                                                                                                                                                                                                         SEQ ID NO 623
LENGTH: 2355
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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                                           GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr
                                                                GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT
                                                                                     TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer
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|TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 220
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US-10-995-901-02.

Sequence 627, Application US/1099561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RU
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOPTWARE: FASTERQ for Windows Version 4.0

SEQ ID NO 627

SEQ ID NO 627

LENGTH: 2355
TYPE: PRT
ORANISM: Homo sapiens
US-10-995-561-627
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Best Local Similarity:
Query Match:
DB:
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US-10-995-561-627
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOPTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1545
LENGTH: 2384
TYPE: PRT
     RESULT 10
US-10-995-561-626
; Sequence 626, Application
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Publication No. US20050255114A1
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis
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Best Local Similarity:
Query Match:
APPLICANT: Ndao, Momar
APPLICANT: Ward, Brian
APPLICANT: Caffrey, Rebecca
APPLICANT: Spithill, Terry
APPLICANT: Li, Hongshan
APPLICANT: Podust, Vladimir
APPLICANT: Perichon, Regis
APPLICANT: Ciphergen Biosystems, Inc.
TITLE OF INVENTION: Serum Biomarkers fo
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US-11-006-119-31
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                                                                                                                  Sequence 31, Application US/11006119 Publication No. US20050260691A1
                                                                                                       GENERAL INFORMATION:
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APPLICANT: CARCILL, Michele et al.

APPLICANT: CARCILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPON

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 626

LEMGTH: 2386

TYPE: PRT

ORGANISM: Homo sapiens

US-10-995-561-626
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                                       550 GAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTTAGCGTTGCTGGT
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                                                                                 GlnProProProTyrGlyHisCysValThrAspSerGlyValValTyrSerValGlyMet
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for Chagas Disease

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Sequence 4, Application US/10631558
Publication No. US20050260598A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Kumar, Rajesh
APPLICANT: Rahani, Girish
APPLICANT: Rajespal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/940,235
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Best Local Similarity:
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PRIOR FILING DATE: 2003-12-05
PRIOR APPLICATION NUMBER: US 60/565,093
PRIOR FILING DATE: 2004-04-22
PRIOR APPLICATION NUMBER: US 60/625,519
PRIOR APPLICATION NUMBER: US 60/625,519
PRIOR FILING DATE: 2004-11-06
NUMBER OF SEQ ID NOS: 38
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ENT APPLICATION NUMBER: US/11/006,119
ENT FILING DATE: 2004-12-06
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                                                                                                                                    SEQ ID NO 632
LENGTH: 693
TYPE: PRT
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Publication No. US20
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/471,349
PRIOR APPLICATION NUMBER: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                        APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
RUMBER OF SEQ ID NOS: 85702
                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                    ORGANISM: Homo
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ORGANISM: Homo
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US-10-995-561-625
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele 
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2004-11-24
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CURRENT ADDITORY.
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CURRENT FILING DATE: 2004-11-24
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Search completed: January 28, 2006, 02:58:11 Job time: 24.1597 secs

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## ALIGNMENTS

streptokinase precursor - Streptococcus "equisimilis" (;Species: Streptococcus "equisimilis" (;Species: Streptococcus "equisimilis" (;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004 (;Accession: A22801 R;Malke, H.; Roe, B.; Ferretti, J.J. Gene 34, 357-362, 1985 Gene 34, 357-362, 1985 A;Title: Nucleotide sequence of the streptokinase gene from Streptococcus et A;Reference number: A22801; MUID:85232082; PMID:2989113 A;Accession: A22801 뮹 δ 밁 S US-09-940-235-11 (1-1782) x A22801 (1-440) Percent Similarity:
Best Local Similarity:
Query Match: C; Superfamily: streptokinase A;Residues: 1-440 <MAL>
A;Cross-references: UNIPROT:P00779; Alignment Scores: A; Experimental source: strain A; Molecule type: DNA Genetics: Хо :: 538 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT 597 47 27 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATC ileAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal 6.23e-140 2158.00 100.00% 100.00% 68.86% H46A UNIPARC: UPI000002BE73; GB: X72832; NID: g407876; Length: Matches: Conservative: Mismatches: Indels: 4440 0 14 0 0 0 0 Streptococcus equisimilis 657 66 46

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A;Residues: 1-415 <JRC>
A;Residues: 10NIPROT:P00779; UNIPARC:UPI0000172BF5
A;Cross-references: UNIPROT:P00779; UNIPARC:UPI0000172BF5
A;Note: 169-Asp and 181-Asp were also found
A;Note: this protein is not a protease, but it activates plasminogen
C;Superfamily: streptokinase
C;Keywords: hydrolase
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(;Speciles: Streptococcus sp.

C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_ch

C;Accession: A00967

R;Jackson, K.W.; Tang, J.

Biochemistry 21, 6620-6625, 1982

A;Title: Complete amino acid sequence of streptokinase and

A;Reference number: A00967, MUID:83127125; PMID:6760891
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Streptokinase G precursor - Streptococcus sp. (strain 1990)
C; Species: Streptococcus sp.
C; Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_cl
C; Accession: S02723
R; Walter, F.; Siegel, M.; Malke, H.
Nucleic Acids Res. 17, 1262, 1989
Nucleic Acids Res. 17, 1262, 1989
A; Title: Nucleotide sequence of the streptokinase gene from A; Reference number: S02723; MUID:89160265; PMID:2922289
A; Accession: S02723
                                                                                                          A;Gene: skg
C;Superfamily: streptokinase
F;1-26/Domain: signal sequence #
F;27-440/Product: streptokinase
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A;Residues: 1-440.<WAL>
A;Cross.references: UNIPROT:P10519;
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TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCCTACAACAATCTC 1557
                                                                                                 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1497
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RESULT 4
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Streptokinase A precursor - Streptococcus pyogenes (strain C;Species: Streptococcus pyogenes
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_cl
C;Accession: S02724
R;Walter, F; Siegel, M.; Malke, H.
Nucleic Acids Res. 17, 1261, 1989
Nucleic Acids Res. 17, 1261, 1989
A;Title: Nucleotide sequence of the streptokinase gene from A;Reference number: S02724; MUID:89160264; PMID:2646590
A;Accession: S02724
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Query Match:
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F;1-26/Domain: signal sequence #
F;27-440/Product: streptokinase
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                             ValArgValArgProTyrLysGluLysProValGlnAsnGlnAlaLysSerValAspVal
                                                  GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
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c;Species: Streptococcus pyogenes
c;Species: Streptococcus pyogenes
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A43867; JU0292
C;Accession: A43867; JU0292
R;Ohkuni, H.; Todome, Y.; Suzuki, H.; Mizuse, M.; Kotani, N.; Horiuchi, K.; Shikama,
                                                                        A;Cross-references: UNIPROT:Q57391; UNIPARC:UPI0000175C82
A;Experimental source: M type 12 strain A374
A;Note: sequence extracted from NCBI backbone (NCBIP:7459)
C;Superfamily: streptokinase
                                                                                                                                                                                Infect. Immun. 60, 278-283, 1992
A;Title: Immunochemical studies and complete amino acid
A;Reference number: A43867; MUID:92104686; PMID:1370275
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  GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                                                                                GluGluProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal
                                                                                                           GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                                                                                                        AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAAGGG
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|PheThTTyrHisIleLysAspArgGluGlnAlaTyrLysAlaAsnSerLysThrGlyIle
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                                                  AspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsn
                                                                                                                                             ValGluLysThrAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLysGly
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S04168
S04168
streptokinase A precursor - Streptococcus pyogenes (streptocics: Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #tc
C;Accession: S04168
R;Huang, T.T.; Malke, H.; Ferretti, J.J.
Mol. Microbiol. 3, 197-205, 1989
A;Title: The streptokinase gene of group A streptococc
A;Reference number: S04168; MUID:89343623; PMID:266868
A;Accession: S04168
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A;Residues: 1-440 <HUA>
A;Cross-references: UNIPROT:Q57391;
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                                   ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
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streptokinase - Streptococcus sp.

C; Species: Streptococcus sp.
C; Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change
C; Accession: S53334
R; Shi, G:Y:; Chang, B:I:; Chen, S:M:; Wu, D:H:; Wu, H:L.
Biochem. J: 304, 235-241, 1994
A; Title: Function of streptokinase fragments in plasminogen act
A; Reference number: S53334
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-197 <SHI>
A; Cross-references: UNIPROT:Q7M115; UNIPARC:UPI000017AC2C
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Pred. No.:
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 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1497
                                                                            AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG 1377
                                                                                                                                         TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 1317
                                                                                                                                                                        TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTACCAATGGATCAAGAG 1257
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SerSerIleVal----------ThrIleLeuproMetAspGlnGlu 94
                                                                                                                                                                                                                                 GCTCAAGCACAAAGCATTTTAAACAAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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                                                           GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 1437
                                                                                                                           PheThrTyr----
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A;Cross-references: UNIPARC:UPI0000000562;
A;Experimental source: strain E2/M3
A;Note: allele 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              streptokinase A (EC 3.4.-.-) (alleles 2 and 3) - Streptococcus pyogenes (fragment) C;Species: Streptococcus pyogenes C;Date: 24-Jul-1998 #sequence revision 24-Jul-1998 #text_change 22-Jun-1999 C;Accession: S77671; S77672 C;Accession: S77671; S77672 Mol. Microbiol. 16, 509-519, 1995 Mol. Microbiol. 16, 509-519, 1995 A;Title: Molecular population genetic analysis of the streptokinase gene of Streptococcu A;Reference number: S77671; MUID:96037795; PMID:7565111 A;Accession: S77671
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S77671
                                                                                                                                                                       US-09-940-235-11 (1-1782) x S77671
                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain A; Note: allele 2
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A; Residues: 1-128 < KAP>
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                                                                                                                                                                                                                                                                                                                      Superfamily: streptokinase
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No.:
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                            GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
                                                                               GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
                                                                                                                                GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
              AspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeu
                                                               GluTyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGlyLeuLys
                                                                                                                    CGTTATACAGGGACACCTATACCTGATAACCCTAACGACAAA 1779
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620.00
95.31%
92.19%
19.78%
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                                                                                                                                                                        (1-128)
                                                                                                                                                                                                                                                                                                         activator; virulence
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Matches:
Conservative:
Mismatches:
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C;Superfamily: streptokinase
C;Keywords: hydrolase; plasminogen
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S77680
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AATGAAGAAATAAACAACACTGAC
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18.16%
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A;Molecule type: DNA
A;Residues: 1-128 <KAP>
A;Cross-references: UNIPROT:Q54687; UNIPARC:UPI00000BD2D3; EMBL:U25862; NID:g818926;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                streptokinase A (EC 3.4.-.-) (allele 11) - Streptococcus pyogenes (fragment C;Species: Streptococcus pyogenes C;Species: Streptococcus pyogenes C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 C;Accession: S77680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTACTTACAGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAATCCTGGTCTG 1317
                                                                                                                          TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
                                                                                                                                                                                                                                   GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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                                                                                                SerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu
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streptokinase A (EC 3.4.-.-) (allele 10) - Streptococcus pyogenes (fragment) C;Species: Streptococcus pyogenes C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 C;Accession: 877679
R;Kapur, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S Mol. Microbiol. 16, 509-519, 1995
A;Title: Molecular population genetic analysis of the streptokinase gene of A;Reference number: 877671; MUID:96037795; PMID:7565111
A;Accession: 877679
A;Status: translation not shown
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A;Residues: 1-128 <KAP>
A;Cross-references: UNITROT:054695;
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A;Title: Molecular population genetic analysis of the streptokinase gene A;Reference number: S77671; MUID:96037795; PMID:7565111
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R; Kapur, V.; Kanjilal,
Mol. Microbiol. 16, 50
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Keywords: hydrolase; plasm
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A;Cross-references: UNIPROT: P02751; UNIPROT
R;Oldberg, A.; Ruoslahti, E.
J. Biol. Chem. 261, 2113-2116, 1986
A;Title: Evolution of the fibronectin gene.
A;Reference number: A26284; MUID:86111901;
                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 31-Dec-2004
C;Accession: A26460; A26284; $03917; A24854; A24476; A91008; A93529; A21011; R;Dean, D.C.; Bowlus, C.L.; Bourgeois, S.
R;Decession: A26460; MUID:87175578; PMID:3031656
R;Accession: A26460; MUID:87175578; PMID:3031656
A;Molecule type: DNA
A;Residues: 1447-1540 <OLD>
A;Cross-references: UNIPARC:UPI0000112E37; GB:M12549; NID:g182688
A;Cross-references: UNIPARC:UPI00000112E37; GB:M12549; NID:g182688
A;Note: the authors translated the codon TTC for residue 1494 as Glu R;Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
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A;Cross-references: UNIPROT:Q54686; UNIPARC:UPI00000B8D6F; EMBL:U25861; NID:g818924;
A;Experimental source: strain ET50/M43
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A; Residues: 1-49 < DEA>
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C;Species: F
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C;Keywords:
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;Keywords: hydrolase; plasminogen
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R;Umezawa, K.; Kornblihtt, A.R.; Baralle, F.E.

FEBS Lett. 186, 31-34, 1985
A;Title: Isolation and characterization of cDNA clones for human liver fibronectin. A;Reference number: A22245; MUID:85231203; PMID:2989004
A;Accession: A22245
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Biochemistry 24, 2698-2704, 1985
B;Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with A;Reference number: A90495; MUID:85280409; PMID:2992573
A;Accession: A90495
                                          Biochemistry 25, 4936-4941, 1986
A;Title: Human liver fibronectin
                                                                                                            A;Cross-references: UNIPARC:UPI0000174332; UNIPARC:UPI0000174333; R;Sekiguchi, K.; Klos, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori,
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J. Biol. Chem. 258, 10193-10196, 1983
A;Title: Molecular cloning and nucleotide sequence of a A;Reference number: AZ1011; MUID:83290929; PMID:6688418
A;Accession: AZ1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 32-1344,1346-2080;2112-2386 <KOR>
A; Residues: 32-1344,1346-2080;2112-2386 <KOR>
A; Cross-references: UNIPARC:UPI000017432E; UNIPARC:UPI000017432F; GB:X02761
R; Kornblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5868, 1984
A; Tille: Human fibronectin: cell specific alternative mRNA splicing generates
A; Tille: Auman fibronectin: cell specific alternative mRNA splicing denerates
A; Reference number: A93529; MUID:84272258; PMID:6462919
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A;Accession: A91008
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A;Cross-references: UNIPARC:UPI000017432D
R;Kornblihtt, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985
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FRBS Lett. 207, 145-148, 1986
A;Title: Human fibronectin is synthesized as a pre-propolypeptide.
A;Reference number: A24476; MUID:87030890; PMID:3770189
A;Accession: A24476
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A;Rosidues: 1594-1767,'V',1769-1783 <PAO>
A;Cross-references: UNIPARC:UPIO00017432B; EMBL:X07718; NID:g31402
A;Note: the authors translated the codon AAC for residue 1631 as Asp
R;Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986
A;Title: Donor and acceptor splice signals within an exon of the human
A;Reference number: A24854; MUID:87030929; PMID:3770201
                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1975-1991;2017-2039 <UM2>
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A;Residues: 1948-2067 <UME>
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A;Residues: 1594-2386 <BER>
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A; Residues: 973-2080; 2112-2386 < KO2>
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A; Residues: 1992-2147 < VIB>
                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI00000046A; GB:M27589; NID:g182705; PIDN:AAA52465.1;
A;Accession: B22245
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liver fibronectin complementary DNAs: identification nber: I52394; MUID:87026578; PMID:3021206
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A; Molecule type: protein
A; Residues: 1614-1630, 'T', 1722-2081, 2113-2244
A; Cross-references: UNIPARC: UPI000017433B
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A;Title: Human plasma fibronectin. Demonstration of structural A;Reference number: S14357; MUID:91190085; PMID:2012601
A;Accession: S14357
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A; Residues: 1589-1630, 'T',1722-2058 <GAR3>
A; Cross-references: UNIPARC: UPI000017433A
R; Tressel, T.; McCarthy, J.B.; Calaycay, J.;
Biochem. J. 274, 731-738, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI0000141CD5
A;Note: residues 1524-1527 are responsible for the cell-binding activity
R;Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
B;Title: Primary structure of human plasma fibronectin. Characterization
A;Reference number: A32517; MUID:87241275; PMID:3593230
A;Accession: A32517
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A;Residues: 291-300;551-560 <GAR2>
A;Cross-references: UNIPARC:UPI0000174337
A;Cross-references: UNIPARC:UPI0000174336; UNIPARC:UPI0000174337
R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3532418
A;Accession: A60904
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, J. Biol. Chem. 260, 10320-10325, 1985
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J. Biol. Chem. 257, 9539-9597, 1982
A;Title: The cell attachment domain of fibronectin.
A;Reference number: A92386; MUID:82265604; PMID:7050
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A; Residues: 616-677, 'Q', 679-703, 'PT' <CAL>
A; Cross-references: UNIPARC: UPI0000174339
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A;Title: Primary structure of a DNA- and heparin-binding domain (domain III) in A;Reference number: A23901; MUID:86008277; PMID:3900070
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A;Residues: 293-301 <GRI>
A;Cross-references: UNIPARC:UPI0000174338
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Arch. Biochem. Biophys. 304, 181-188, 1993
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A;Residues: 32-47,'C',49-51,'S',53-72,'A',74-290 <GAR1>
A;Cross-references: UNIPARC:UPI0000174335
R;Garcia-Pardo, A.; Gold, L.I.
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A;Status ----
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J. Biol. Chem. 258, 12670-12674, 1983
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A; Residues: 2291-2386 < KO3>
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A; Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 <SEK>
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A;Accession: A92398
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PMID:6630202
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of human plasma fibronectin.

Characterization of a 31,000-da

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F;52-87/Domain: fibronectin type I repeat homology <1F1>
F;97-115/Domain: fibronectin type I repeat homology <1F2>
F;141-179/Domain: fibronectin type I repeat homology <1F3>
F;186-225/Domain: fibronectin type I repeat homology <1F4>
F;186-225/Domain: fibronectin type I repeat homology <1F4>
F;231-270/Domain: fibronectin type I repeat homology <1F5>
F;308-408/Domain: collagen binding <CBR>
F;308-442/Domain: fibronectin type I repeat homology <2F1>
F;308-441/Domain: fibronectin type II repeat homology <2F1>
F;470-461/Domain: fibronectin type II repeat homology <2F2>
F;470-508/Domain: fibronectin type I repeat homology <1F8>
F;518-555/Domain: fibronectin type I repeat homology <1F8>
F;561-599/Domain: fibronectin type I repeat homology <1F8>
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F;32-2386/Product: fibronectin #status experimental <MAT>
F;52-272/Domain: fibrin and heparin binding <FHB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: acute phase; alternative spitching; control F;1-26/Domain: signal sequence #status predicted <SIG>
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A;Introns: 49/3; 1266/1; C;Superfamily: fibronecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UPI000017433C; UNIPARC:UPI000017433D
C;Comment: The extra domain and connecting strand 3 are subject to developmental and tin
C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins
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A;Accession: A23891
A;Molecule type: protein
A;Residues: 2071-2080;2112-2356 <GAR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-940-235-11
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            GlnTrpLeu----
                                                             GAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTTAGCGTTGCTGGT
                                                                                                                       GlnProProTyrGlyHisCysValThrAspSerGlyValValTyrSerValGlyMet
                                                                                                                                                                                                                                                                             AGCGGATCTGGCCCCTTCACCGATGTTCGTATTGCT------
                                                                                                                                                                                                                                                                                                                                                            AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
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63.12%
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                                                                                                 A, Residues; 1-16, (°, 18-20, °s, 22-432;447-463;1367-1517;1567-1673;2062-2176, 'N', 2178-226 A, Residues; 1-16, (°, 18-20, °s, 22-432;447-463;1367-1517;1567-1673;2062-2176, 'N', 2178-226 A, Cross references: UNIPARC:UPI0000174338; UNIPARC:UPI0000174339; CNIPARC:UPI0000174340; Cycomment: Cys-1201 and Cys-2015 have free sulfhydryl groups.

Cycomment: Plasma fibronectin bind cell surfaces and various compounds including collagen, fill cycomment: Plasma fibronectin; is symthesized by hepatocytes.
Cycomment: Plasma fibronectin; fibronectin type I repeat homology; fibronectin type II repeat homology; fibronectin type II repeat homology cycomment.
Fig. 1-26, Cybomain: Fibronectin type I repeat homology cycomment.
Fig. 1-24, Domain: fibronectin type I repeat homology cycomment.
Fig. 1-25, Cybomain: fibronectin type I repeat homology cycomment.
Fig. 1-25, Cybomain: fibronectin type I repeat homology cycomment.
Fig. 1-27-57/Domain: fibronectin type II repeat homology cycomment.
Fig. 1-27-57/Domain: fibronectin type II repeat homology cycomment.
Fig. 1-27-57/Domain: fibronectin type II repeat homology cycomment.
Fig. 1-27-57/Domain: fibronectin type III repeat homology cycomment.
Fig. 1-27-57/Domain: fibronectin type III repeat homology cycomment.
Fig. 1-27-1318/Domain: fibronectin type III repeat homology cycomment.
Fibronectin type III repeat homology
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A; Residues: 1-2265 < SKO>
A; Cross references: UNIPROT: P07589; UNIPARC: UPI000012A7E
A; Cross references: UNIPROT: P07589; UNIPARC: UPI000012A7E
R; Kornblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A; Title: Isolation and characterization of cDNA clones f
A; Reference number: A21165; MUID: 83221567; PMID: 6304699
A; Accession: B21165
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A;Title: Complete primary structure of bovine plasma fi.
A;Reference number: A26452; MUID:87054047; PMID:3780752
A;Accession: A26452
                              F;1985-2216/Domain:
F;2085-2124/Domain:
                                                                                        F;1982-2062/Domain:
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fibronectin type III a fibrin binding <FB2> fibronectin type I rep fibronectin type I rep
I repeat homology <1F10>
I repeat homology <1F11>
                                                                                     III repeat
                                                                                        homology
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<FN30>

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A;Molecule type: mRNA
A;Residues: 2170-2265 <KOR>
A;Residues: 2170-2265 <KOR>
A;Cross-references: UNIPARC:UPI000016C30C; GB:K00800; NID:g163055; PIDN:AAA30521.2; PID.
A;Cross-references: UNIPARC:UPI000016C30C; GB:K00800; NID:g163055; PIDN:AAA30521.2; PID.
R;Petersen, T.E.; Thogersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sott:
Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 198
Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 198
A;Reference number: Az3292; MUID:83117805; PMID:6218503
A;Accession: A23292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26452; B21165; A23292
R;Skorstengaard, K; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S. Bur. J. Biochem. 161, 441-453, 1986
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K.; Baralle, F.E.
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-2477 < HYN>
A; Cross-references: UNIPROT: P04937; UNIPARC: UPI000012A7C6;
A; Cross-references: UNIPROT: P04937; Fonda, D.; Hynes, R.O.
                                                                                                                                                                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Cross-link: isopeptide (Gln) (Interchain to Lys N6-amino of fibrin) #status experime
F;21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,302-3
7,2155-2167,2174-2200,2198-2209/Disulfide bonds: #status predicted
F;399,497,511,846,976,1213,1987/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;1205,1692/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;1243,1944/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;2246/Disulfide bonds: interchain (to 2250) #status predicted
F;2250/Disulfide bonds: interchain (to 2246) #status predicted
                                      R;Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O. EMBO J. 6, 2573-2580, 1987
A;Title: Multiple sites of alternative splicing of the rat A;Reference number: S12455; MUID:88054951; PMID:2445560
                                                                                                                                                                                                                  submitted to the EMBL Data A; Reference number: S14428
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                        A; Accession: S12455
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2 7 8
                                                              fibronectin
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                                                            gene
                                                                                                                             NID:g56163;
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                                                              transcript.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1722-1810 < RES >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A27252;
A;Accession: A27252
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F;142-180/Domain: fibronectin type I repeat homology <1F3>
F;187-226/Domain: fibronectin type I repeat homology <1F4>
F;232-271/Domain: fibronectin type I repeat homology <1F4>
F;308-342/Domain: fibronectin type I repeat homology <1F6>
F;308-342/Domain: fibronectin type II repeat homology <1F6>
F;360-401/Domain: fibronectin type II repeat homology <2F1>
F;470-508/Domain: fibronectin type II repeat homology <2F2>
F;470-508/Domain: fibronectin type II repeat homology <1F8>
F;518-555/Domain: fibronectin type II repeat homology <1F9>
F;518-592/Domain: fibronectin type III repeat homology <1F9>
F;518-692/Domain: fibronectin type III repeat homology <FN3B>
F;108-890/Domain: fibronectin type III repeat homology <FN3B>
F;809-897/Domain: fibronectin type III repeat homology <FN3B>
F;995-1076/Domain: fibronectin type III repeat homology <FN3B>
F;1085-1164/Domain: fibronectin type III repeat homology <FN3F>
F;1172-1257/Domain: fibronectin type III repeat homology <FN3G>
F;1265-1348/Domain: fibronectin type III repeat homology <FN3G>
F;1356-1348/Domain: fibronectin type III repeat homology <FN3G>
F;136-1349/Domain: fibronectin type III repeat homology <FN3G>
F;136-1439/Domain: fibronectin type III repeat homology <FN3G>
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1183-1192; 'GLN', 1268, 'p', 1270-1271, 'D', 1273, 'CF', 1276, 'PY'; 1385-1399 <FAL>
A; Cross-references: UNIPARC: UDIO000177AEC; UNIPARC: UDIO000177AED; UNIPARC: UDIO000177AEE
R; Pattel, R.S.; Odermatt, E.; Schwarzbauer, J.E.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1987
A; Title: Organization of the fibronectin gene provides evidence for exon shuffling duri
A: Deference number: S00459; MUID:88054950; PMID:3119323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;33-2477/Product: fibronectin #status predicted <MAT>
F;53-88/Domain: fibronectin type I repeat homology <1F1>
F;98-136/Domain: fibronectin type I repeat homology <1F2>
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Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A;Title: Repeating modular structure of the fibronectin gene: Relationship
A;Reference number: I59049; MUID:86016741; PMID:3863113
A;Accession: I59049
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Cell 35, 421-431, 1983
A;Title: Three different fibronectin mRNAs
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A;Residues: 1-139;2382-2477 <PAT>
A;Residues: 1-139;2382-2477 <PAT>
A;Cross-references: UNIPARC:UPI000017095C; UNIPARC:UPI0000177AEF;
A;Note: the authors translated the codon CCT for residues 51 and :
A;Note: the authors translated the codon CCT for residues 51 and :
R;Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 2052-2237 <TAM>
A;Coss-references: UNIPARC:UPI0000177AEB
R;Falkenberg, C.; Enghild, J.J.; Thogerser
Biochem. J. 301, 745-751, 1994
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R;Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A;Title: A single rat fibronectin gene generates three different mRNAs by alternative A;Reference number: A22319; MUID:84298097; PMID:6089177
A;Accession: A22319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: fibronectin; fibronectin type I r. C; Keywords: alternative splicing; cell adhesion;
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A;Residues: 1586-1720,'T',1722,1813-2477
A;Cross-references: UNIPARC:UPI0000177AF0
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lcing; cell adhesion; collagen binding; disulfide bond; dupl
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streptokinase A (EC 3.4...-) (allele 7) - Streptococcus pyogenes (fragment)
C;Species: Streptococcus pyogenes
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S77676
C;Accession: S77676
R;Kapur, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser, Mol. Microbiol. 16, 509-519, 1995
A,Title: Molecular population genetic analysis of the streptokinase gene of Streptococcu A;Reference number: S77671; MUID:96037795; PMID:7565111
A;Accession: S77676
A;Status: translation not shown
A;Molecula type: DNA
A;Molecula type: DNA
A;Molecula type: DNA
A;Residues: 1-128 <KAP>
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F;1614-1616/Region: cell attachment (R-G-D) motif
F;1631-1713/Domain: fibronectin type III repeat homology <FN3L>
F;1631-1713/Domain: fibronectin type III repeat homology <FN3M>
F;1721-1803/Domain: fibronectin type III repeat homology <FN3N>
F;1903-1984/Domain: fibronectin type III repeat homology <FN3N>
F;1992-2074/Domain: fibronectin type III repeat homology <FN3P>
F;1992-2074/Domain: fibronectin type III repeat homology <FN3P>
F;2181-2183/Region: cell attachment (R-G-D) motif
F;2193-2273/Domain: fibronectin type III repeat homology <FN3Q>
F;2181-2378/Domain: fibronectin type I repeat homology <1F10>
F;2341-2378/Domain: fibronectin type I repeat homology <1F11>
F;2341-2378/Domain: fibronectin type I repeat homology <1F12>
F;3341-2378/Domain: fibronectin type I repeat homology <1F12>
F;3341-2378/Domain: fibronectin type I repeat homology <1F12>
F;335-79,77-88,98-126,714-136,742-170,168-180,187-216,214-226,232-261,259-271,308-335,333
366,2366-2378,2385-2411,2409-2420/Disulfide bonds: #status predicted
F;2458/Disulfide bonds: interchain (to 2462) #status predicted
F;2462/Disulfide bonds: interchain (to 2458) #status predicted
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                           GlnTrpLeu-----LysSerGlnGlyAspLysGlnMetLeuCysThrCysLeuGly
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57.50%
14.50%
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Indels:
Gaps:
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Matches:
Conservative:
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Search completed: January 28, Job time: 44.3089 secs

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-DB-Unifrot -QFWT=fastan -SUFFIX=rup -MINWATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MRTX=blosum62 -TRANS-buman40.cdi -LIST=45
-DCCALIGN=200 -THK SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-USER-US09940235 @CGN 1 11359 @runat 27012006 144218 27563 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 :WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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## RESULT 1 STRP\_STRI STREQ STREO STANDARD; ALIGNMENTS 440 Ą

STRP\_STI P00779; 21-JUL-1986 (Rel. 01, Crea 01-APR-1988 (Rel. 07, Last 10-MAY-2005 (Rel. 47, Last Streptokinase C precursor. Last Last Created) annotation update) sequence update)

Streptococcus equisimilis. Name=8kc;

NCBI\_TaxID=119602; Streptococcus Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

MEDLINE=85232082; PubMed=2989113; DOI=10.1016/0378-1119(85)90145-3; Malke H., Roe B.A., Ferretti J.J.; "Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A."; **3ene 34:357-362(1985).** 

NUCLEOTIDE SEQUENCE.

PROTEIN SEQUENCE OF 27-440. MEDLINE=83127125; PubMed=6760891;

Jackson K.W., Tang J.; "Complete amino acid sequence of streptokinase and its homology with

serine proteases.";

Biochemistry 21:6620-6625(1982).

-!- FUNCTION: This protein is not a protease, but it activates plasminogen by complexing with it. As a potential virulence factor, it is thought to prevent the formation of effective barriers around the site of infection, thereby contributing invasiveness of the cells. fibrin to the

the This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics Institute. There are no restitute the complete of the complete content 18 ä ᄗ way modified There are this restrictions EMBL outstation statement a collaboration 18

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PIR; A22801, A22801.
PDB; 11ML; X-ray; C/D=38-399.
PDB; 114D; X-ray; B=40-173.
PDB; 114Z; X-ray; B=27-173.
PDB; 114Z; X-ray; B=27-173.
PDB; 10QR; X-ray; A/B/C/D=177-314.
SMR; P00779; 38-398.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR008124; Streptokinase.
Pfam; PF02811; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
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PDB; 1C4P; X-ray; A/BC/D=149-285.

RSMR; Q53284; 12-372.

RSMR; Q53284; 12-372.

RGO; GO:0005515; F:plasminogen activator activity; IEA.

RGO; GO:0005515; F:protein binding; IEA.

InterPro; IPR004093; Staphylokinase.

InterPro; IPR004093; Staphylokinase.

InterPro; IPR008124; Streptokinase.

R InterPro; IPR008124; Streptokinase.

R FARM; PF02821; Staphylokinase.

R FARM; PF02821; Staphylokinase.

R FRINTS; PR01753; STREPKINASE.

R PRINTS; PR01753; STREPKINASE.
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Streptococcus
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Mismatches:
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                                                                    STRAIN-ATCC 35666;

Costa C.S., Torres F.A.G., Filho S.A.;

R Costa C.S., Torres F.A.G., Filho S.A.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ da

R EMBL; AY368335; AAQ73571.1; -; Genomic_DNA.

R SNR; Q6UK57; 59-394.

R GO; GO:0016301; F:kinase activity; IEA.

R GO; GO:0016301; F:plasminogen activator activity

R GO; GO:0008243; F:plasminogen activator activity

R GO; GO:0008515; F:protein binding; IEA.

R InterPro; IPR004093; Staphylokinase.

R InterPro; IPR004124; Streptokinase.

Pfam; PF02821; Staphylokinase; 3.

PFam; PF02821; Staphylokinase; 3.

PRINTS; PR01753; STREPKINASE.
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STREQ
Q6UK57 STREQ 1
Q6UK57;
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NCBI_TaxID=119602;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
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                                                      AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAAGGG
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                                                                                                                                                                                AlaGlnAlaGlnSerIleLeuAsnLysThrHisProGlyTyrThrIleTyrGluArgAsp
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RESULT 4

STRP STRS1

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AC P10519;

DT 01-UUL-1989

DT 01-UUL-1989

DT 13-SEP-2005

DE Streptococci

OC Streptococci

OX NCBI TaxID=

OC NCBI TaxID=

RA WALLET F. (2)

RA WALLET F. (2)

RA WALLEOTIDE (2)

RA WALLEOTIDE (2)

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PIR; S02723; S02723.
HSSP; P00779; 1QQR.
SMR; P10519; 63-398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus., Streptococcus., Streptococcus., Streptococcus., Nucleic Acids Res. 17:1262-1262(1989).

Nucleic Acids Res. 17:1262-1262(1989).

Plasminogen by complexing with it. As a potential virulence factor, it is thought to prevent the formation of effective barriers around the site of infection, thereby contributing invasiveness of the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA]
MEDLINE=89160265; PubMed=2922269;
Malter F., Siegel M., Malke H.;
                                                                                                                                                                                                                 Plasminogen activation; Signal; Virulence SIGNAL 1 26 CHAIN 27 440 Streptokinas
                                                                                                                                                                                                                                                                                              InterPro; IPR004093; Staphylokinase
InterPro; IPR008124; Streptokinase.
Pfam; PF02821; Straphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
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Name=skg;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s Swiss-Prot entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1618
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"Natural selection and evolution of streptoco involved in tissue-specific adaptations.";

J. Bacteriol. 186:110-121(2004).

EMBL; AV234117; AAP39957.1; -; Genomic DNA.

HSSP; Q53284; 1C4P.

SMR; Q7X0Y1; 63-398.

GO; GO:0016301; F: kinase activity; IEA.

GO; GO:0016301; F: plasminogen activator activ GO; GO:0008244; F: plasminogen activator activ GO; GO:0005515; F: protein binding; IEA.

InterPro; IPR004093; Staphylokinase.

InterPro; IPR004124; Streptokinase.

Pfam; PF02821; Staphylokinase; 3.

PRINTS; PR01733; STREPKINASE.

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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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(STRAIN=SF370 / ATCC 700294 / Serotype Mi].

(STRAIN=SF370 / ATCC 700294 / Serotype Mi].

(X MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;

(X MEDLINE=21192684; PubMed=112106296; DOI=10.1073/pnas.071559398;

(X MEDLINE=21192684; PubMed=11206296; DOI=10.1073/pnas.071559398;

(X Perretti J.J., McShan W.M., Ajddc D.J., Savic D.J., Savic G., Lyon I.

(A Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

(A Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

(A Qian Y., Clifton S.W., Roe B.A., McLaughlin R.E.;

(T "Complete genome sequence of an M1 strain of Streptococcus pyogenes.

(T "Complete genome sequence of an M1 strain of Streptococcus pyogenes.

(L Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

(2 - FUNCTION: This protein is not a protease, but it activates plasminogen by complexing with it. As a potential virulence factor, it is thought to prevent the formation of effective fib.

(2 barriers around the site of infection, thereby contributing to the strain of the site of infection of the strain of the site of infection.)
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EMBL; AE006620; AAK34665.1; -; Genomic DNA.
PIR; S02724; S02724.
HSSP; Q53284; 1C4P.
SMR; P10520; 63-398.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR008124; Streptokinase.
Pfam; PP02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
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STRAIN-SF130/13 / Serotype M1;

WEDLINE=89160264; PubMed=2646590;

Walter F., Siegel M., Malke H.;

"Nucleotide sequence of the streptokinase pyogenes type 1 strain.";

Nucleic Acids Res. 17:1261-1261(1989).

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PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;

Ralia A., Bessen D.E.;

Kalia A., Beslection and evolution of streptococcal v.

involved in tissue-specific adaptations.";

J. Bacteriol. 186:110-121(2004).

EMBL; AY234128; AAP39948.1; -; Genomic_DNA.
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QBK5R8 STRP3 PRELIMINARY;

QBK5R8; Q79W73;

Q1-QCT-2002 (TrEMBLrel. 22;

Q1-QCT-2005 (TrEMBLrel. 31;

Streptokinase A.
NUCLEOTIDE SEQUENCE.
STRAIN-MGASJIS / Serotype M3;
MEDLINE-22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococo
phage-encoded toxins, the high-virulence phenotype, and clone
emergence.";
                                                                                                                                                                                                                                                                         Name=ska; OrderedLocusNames=SPs1700, Sp
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales;
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Genome Res. 13:1042-1055 (2003).

EMBL; BR014169; AAM80305.1; -; Genomic_DNA.

EMBL; BA000034; BAC64795.1; -; Genomic_DNA.

HSSP; P00779; 114D.

SMR; Q8X5R8; 63-398.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:008243; F:plasminogen activator activity; IEA.

GO; GO:0008215; F:protein binding; IEA.

InterPro; IPR004093; Staphylokinase.

InterPro; IPR004093; Staphylokinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.
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GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 1137

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RESULT 9
ID Q7XOY2_STRPY P
AC Q7XOY2;
TD Q7XOY2;
DT 01-CCT-2003 (T
DT 01-MAR-2004 (T
DT 01-MAR-2004 (T
DT Streptococcus
GN Name-ska;
OS Streptococcus
OS Streptococcus
OX NCBI_TaxID=131
RN NUCLEOTIDE SEQ
RC STRALN=1306;
RX PLDMed=1467923
RA Kalia A. Bessa
RT "Natural selectiol.
DR MSP; Q53284;
DR SMR; Q7XOY2; 6
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01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
Streptokinase.
"Natural selection and evolution of streptococcal virulence involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).

EMBL; AY23413; AAP39956.1; -; Genomic_DNA.

HSSP; O53284; 1C4P.

SMR; Q7X0Y2; 63-398.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0008243; F:plasminogen activator activity; IEA.
                                                     PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004; Kalia A., Bessen D.E.;
                                                                          NUCLEOTIDE SEQUENCE
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InterPro; IPR004093; Staphylokinase:
InterPro; IPR008124; Straptokinase.
Pfam; PF02821; Staphylokinase; 3.
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SMR; 07X0Y8; 63-398.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator ac
GO; GO:0005515; F:protein binding; IEA.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR004124; Streptokinase.
Pfam; PF02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
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01-OCT-2003 (TrEMBLrel. 2
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J. Bacteriol. 186:110-121(2004).
EMBL; AY234129; AAP39949.1; -; Genomic_DNA.
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      IleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAsp

   GluSerProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal
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SMR; Q7X0Y7; 63-398.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator ac
GO; GO:0008515; F:protein binding; IEA.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR008124; Streptokinase.
Pfam; PP02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
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01-MAR-2004 (TrEMBLrel.
Streptokinase.
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PubMed=14679231; DOI=10.1128/JB.186.1.110-121.
Kalia A., Bessen D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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J. Bacteriol. 186:110-121(2004).

EMBL; AY234130; AAP39950.1; -; Genomic_DNA.

HSSP; Q53284; 1C4P.
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ZEMBL; CP000003; AAT87827.1; -; Genomic_DNA.

RMR; Q5X976; 63-398.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0008243; F:plasminogen activator activity; IEA.

GO; GO:0005215; F:protein binding; IEA.

RINTERPRO; IPR004093; Staphylokinase.

R InterPro; IPR004093; Staphylokinase.

R InterPro; IPR008124; Streptokinase.

R Pfam; PF02821; Staphylokinase; 3.

R PRINTS; PR01753; STREPKINASE;

Complete proteome; Hydrolase; Kinase.

Complete proteome; Hydrolase; Kinase.
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OrderedLocusNames=M6_Spy1692;
Streptococcus pyogenes (serotype M6).
Bacteria; Pirmicutes; Lactobacillales; Streptococcaceae;
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PubMed=15272401; DOI=10.1086/422697;
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Streptokinase
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STRAIN-MGAS832 / Serotype M18;

MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;

Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;

"Genome sequence and comparative microarray analysis of serotype group A Streptococcus strains associated with acute rheumatic fev
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HSSP; OS3284; 1C4P.
SMR; Q8NZA6; 63-398.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator ac
GO; GO:0005515; F:protein binding; IEA.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR004093; Streptokinase.
Pfiam; PF02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
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J. Bacteriol. 186:110-121(2004).
EMBL; AY234134; AAP39954.1; -; Genomic_DNA HSSP; Q53284; 1C4P.
SWR; Q7X0Y3; 63-398.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator ac GO; GO:0008243; F:protein binding; IEA.
InterPro; IPR008124; Staphylokinase.
InterPro; IPR008124; Streptokinase.
Pfam; PP02821; Staphylokinase; 3.
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STRAIN=ALAB49;
PubMed=14679231; DOI
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01-OCT-2003 (TrEMBLrel.
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                                                                                           SEQUENCE
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NCBI_TaxID=1314;
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J. Bacteriol. 186:110-121(2004).

EMBL; AY234138; AAP39958.1; -; Genomic_DNA.

HSSP; O53284; 1C4P.
SMR; Q7X0Y0; 63-398.

GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator activ.
GO; GO:0008243; F:plasminogen activator activ.
GO; GO:0008243; F:protein binding; IEA.

InterPro; IPR004093; Staphylokinase.
InterPro; IPR008124; Streptokinase.
Pfam; PF02821; Staphylokinase.
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Bacteria; Firmicutes; Lactobacillales;
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AT 1677    Yr 406	8 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAA        :::::                        7 ASDASDATGValValThrValTyrMetGlyLy8ATgProLy8
AC 1617 Ys 386	8 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAA            7 AspAlaPheAspIleMetAspTyTThrLeuThrGlyLy
TC 1557    eu 366	98 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCCTACAACA 
14 34	1438 GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC             327 AspValAspThrLysAlaLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsn
14 32	1378 GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT    :::
1377       361y 306	18 AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAA    :::
CTG 1317 ::: ::: 286	1258 TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTC 
AG 12 	98 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAC 
11 24	38 GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAAC 
TA 1137     eu 226	78 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCAC 
AA 1077    Nys 206	18 GAATATACTGTA
TG 1017 :: le 186	8 GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATG 
AT 957     is 166	898 AAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGAATTTTTGCTAAGCGGACA :::
AC 897 :: .sn 146	838 ATTGATITTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTG
TC 837	778 AAGGCTATTCAAGAACAATTGATGGCTAACGTCCACAGTAACGACGACTACTTTGAGGT 
TA 777	18 AAACCATTT          87 LysProPhe

Search completed: January 28, 2006, 02:34:10 Job time : 211.043 secs

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1 cgaagaccattcatgttgtt.....ccttcaccgatgttcgttag 2096
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	1121 4	1122.2	1122.4	1122.4	1122.4	1122.4	1124.6	1124.6	1125.4	1125.4	1132.4	1139	1141.6	1145.4	1146.4	1146.4	1146.4	1150.8	Score
	N N	53.5	53.5	53.5	53.5	53.5		53.7	53.7	53.7	54.0	.54.3	54.5	54.6	54.7	54.7	54.7	54.9	Query
100	1357	2589	1512	1512	1335	1335	7057	1245	1458	1458	2566	1401	2568	1242	8931	2568	2568	2385	Length
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AZOULS SEC 10 NO:			I13204 Sequence 27	A20016 SEQ ID NO:	I13194 Sequence 14	A20006 SEQ ID NO:	CQ797820 Sequence	S46536 SKC-2=strep	I13215 Sequence 42	A20027 SEQ ID NO:	AR068768 Sequence	I05204 Sequence 5	E00522 DNA fragmen	AR144000 Sequence	X72832 S.equisimil	A04926 S.equisimil	K02986 Streptococc	AR143998 Sequence	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19
1005.6	1012	1013.6	1013.6	1013.6	1013.6	1064	1075.8	1076	1077.2	1086	1086	1086	1086	1093.6	1093.6	1093.6	1093.6	1112.8	1114.4	1116.6		1121.4	1121.4	1121.4	1121.4	1121.4
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## ALIGNMENTS

RESULT 1

AGTAACGAC 872	CTAACGTCCAC	813 AAAGCTGACTTACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGAC	Qy 81
AAACTTGAG 812         AAACTTGAG 1368	CGCGATGTCACAT.             GCGATGTCACAT	753 TTAAGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAG 	Qy 753 Db 1309
GAGCAAGGC 752          GAGCAAGGC 1308	TGGAGGAAAGACA            TGGAGGAAAGACA	693 AAATTTTTTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGG 	Qy 693 Db 1249
ATTAGTCTT 692          ATTAGTCTT 1248	GACGAATCAAGAC           JACGAATCAAGAC	633 AGCCAATTGGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTT 	Qy 633 Db 1189
GTCAACAAC 632         GTCAACAAC 1188	AGACCGTCCATCT          AGACCGTCCATCT	573 TTCACCGATGTTCGTATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAAC	Qy 573 Db 1129
0; Gaps 0;	; Length 23 Indels	/ Match 54.9%; Score 1150.8; DB 6; Local Similarity 99.0%; Pred. No. 7.7e-299; les 1158; Conservative 0; Mismatches 12;	Query Match Best Local Si Matches 1158;
	ctivator		KEYWORDS SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE TITLE TOURNAL FEATURES SOURCE ORIGIN
PAT 08-AUG-2001	linear p	AR143998 2385 bp DNA Sequence 1 from patent US 6210667. AR143998 1 GI-15105865	AR143998 LOCUS DEFINITION ACCESSION VERSION

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STRSKC 2568 bp I Streptococcus equisimilis (H46A) str K0298  
K02986.1 GI:153808  
K02986.1 GI:153808  
Streptococcus dysgalactiae subsp. eq Streptococcus dysgalactiae subsp. eq
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The -35 and -10 regions are located at positions 760-765 and 781-786 respectively and an SD sequence at 808-813. Downstream from the coding region inverted repeats (positions 2176-2190 and 2203-2217) are thought to function as transcription terminators. The nucleotide sequence of skc does not support the hypothesis that the gene has evolved by duplication and fusion, as suggested by internal two-fold AA homologies of its product.
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equisimilis H46A
Gene 34 (2-3), 357-362 (1985)
                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                 CATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                        upstream of PstI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="streptokinase signal peptide"
897. .2138
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819. .2141
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/db_xref="GI:153809"
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/mol_type="genomic DNA"
/db_xref="taxon:119602"
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of the streptokinase
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Pred. No. 1.2e-297;
0; Mismatches 6;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
1 (bases 1 to 2568)
Malke, H., Roe, B. and Ferretti, J.J.
from
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Original source text: S.equisimilis (strain H46A) DNA, Draft entry and hard copy of sequence for [1] kindly p. J.J.Ferretti, 03-SEP-1985. A, clone p pMF5

dysgalactiae subsp. equisimilis'

tränslation="MKNYLSFOMFALLFALTFOTVNSVQAIAGERMILDRESVNNSQL VVSVAGTVEGTNQDISLKFFEIDLTSRPAHGKTEQGLSFKSKEPATDSGAMSHKLEK ADLIKALQEQLIANVISHODVEEVIDEASDATITDRNGKVYFADKOGSVTLFTQPVQE FILSGHVRVRPYKEKFIQNQAKSVDVEYTVQFTPLNPDDDFRGLKOTKLLKTLAIGD FILSGHVRVRPYKEKFIQNQAKSVDVEYTVQFTPLNPDDDFRGLKOTKLLKTLAIGD TITSQELLAQAGSILMKNHPGYTIYEROSSIVTDNDIFFTILLEMDQBETYRVKNREQ AYRINKKSGLAKEEINNTDLISEKYVYLKKGEKVDDPFDRJLKLFTIKKVDDTVNLI AYRINKKSGLAKEEINNTDLISEKSVYLKKGKFOMDYTLTGKVEDNHDDTNRIIT VYMGKRPEGENASYHLAYDKDRYTEEEREVYSYLRYTGTPI PDNPNDK"

Length 2568; 0, Gaps 646 0

TATTGCTGGACCTGAGTGGCTAGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGT CGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATC CGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATC TAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAAT TATTGCTGGACCTGAGTGGCTAGACCGTCCATCTGTCAACAACAGCCAATTAGTTGT 1075 766 1015 706 955

CATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGA AAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGT AAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGT AAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACT AAAACCATTTGCTACTGATAGTGGCGCGCATGTCACATAAACTTGAGAAAAGCTGACTTACT 1255 946 1195 1135 886 826

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S.equisimilis skc gene for streptokinase.
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A04926.1 GI:412219
streptokinase.
Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
Streptococcus dysgalactiae subsp. equisimilis
1 (bases 1 to 2568)

Ferretti,J.J. and Malke,H.

Streptokinase-coding recombinant vectors

Patent: EP 0151337-A 1 14-AUG-1985;

THE BOARD OF REGENTS OF THE UNIVERSITY OF
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                      GGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGT
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                                                                                                                                                              CTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGA
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/mol_type="unassigned DNA"
/sub_species="equisimilis"
/db_xref="taxon:119602"
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99.5%;
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Mechold, U., Steiner, K., Vettermann, S. and Malke, H
Genetic organization of the streptokinase region
Streptococcus equisimilis H46A chromosome
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abc gene; ABC transporter; dexB gene; dextran glucosidase; glucan 1,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel gene; skc gene; streptokinase; stringent response-like protein. Streptococcus dysgalactiae subsp. equisimilis streptococcus dysgalactiae subsp. equisimilis
                                                                                                                                                                                                                                                                                                                                                          Submitted (05-MAY-1993) H. Malke, Institute for Molecular Jena University, Winzerlaer Str 10, 07708 Jena, FRG Related sequences: K02986, M19346, X13399 & X13400.

Location/Qualifiers
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                                                                                                                                                    /chromosome="streptokinase region"
/clone lib="E.coli plasmid library containing subfragments
of the submitted seq:pSHD14/16, pSPV19, pSH2, pMF1,
pCWP73, pRH10, pWX4"
complement(89. .1761)
                                                                    /note="hairpin loop"
complement (136. .1749)
                                                                                                       /gene="dexB"
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/mol_type="genomic DNA"
/strain="H46A"
/codon_start=1
/transl_table=11
                                                      'gene="dexB"
                                                                                                                                     /gene="dexB"
                                                                                                                                                                                                                                          isolate="human group C strain"
sub_species="equisimilis"
db_xref="taxon:119602"
                                    _number="3.2.1.70"
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LAILLHLMRGTFYYYQGEEIGMTNYPFKDLTEVDDIESLNYAKEAMENGVPAARVMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (2828. .2854)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (1757. .1761)
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                                                                                                      complement (3244.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (2644)
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                                                                                                                                                                                                                                            complement (3043.
                                                                                                                                                                                                                                                                                                                                                        /gene="abc"
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complement(2973. .2976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="abc"
/note="(+1) frame
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                                                                                                                                   note="TG motif"
                                                                                                                                                               'gene="abc"
                                                                                                                                                                                                                                                                         note="alternative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Walker motif B"
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                                                                                                            .4149)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="6
                                                                                                    /replace="gc" 6162. .6164
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    complement (6317.
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4439. .5761
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4401. .4406
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QMIAGLEVILP ISTTQTAFLCRQATS IKVLESLEGILFTLESDEDLALTMFVGRAMYQ
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                                                                                                                                                                                                                                                                                                                                                                                                    /note="unnamed
                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="skc"
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/note="alternative"
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4392. .4393
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4392. .5837
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complement(4117. .4120)
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CTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCT 1606
                                        TGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAA
                                                                                                                                                              GGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGT 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTCAAGCACAAAGCATTTTAAACAAAAAACCACCAGGCTATACGATTTATGAACGTGA 1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACA 1006
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                                                                                                                          GGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGT
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Pred. No. 1.36
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Best Local Similarity
Matches 1149; Conserv
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Bacterial fibrin-dependent plasminogen
Bacterit: US 6210667-A 5 03-APR-2001;
Patent: US 621067/Qualifiers
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Sequence 5 :
AR144000
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GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 1127
                        GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
                                         GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
                                                                                  AAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
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PRECOMBINATION VECTOR FOR PRODUCING STREPTOKINASE
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PHILLIPS PETROLEUM CO

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JP 1985237955-A/1.
Streptcococus dysgalactiae subsp. equisimilis
Streptcococus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobaciliales; Streptococcaceae;
          PF 09-OCT-1984 JP 1984212403
PR 10-OCT-1983 DD 83 255523, 02-MAR-1984 US 84 585417 PI
JIYOSEFU JIEI FUERTISUTEI, HORUSUTO MARUKE
PC C12N15/00,C12N1/20,C12N9/70,(C12N15/00,C12R1:46),(C12N1/20,
                                                                                                                                                                                                                                                                                            DNA fragment
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CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: strain=Streptococcus equismilis H46A; CC library=streptococcus equismilis H46 library; CC *source: strain=Streptococcus equismilis H46 library; CC *source: strain=Streptococcus equismilis H46 library; CC *sou clone=lambda L47 skc clone;
FH Key Location/Qualifiers
FT 5'UTR 1. .818
FT 5'UTR 819. .896
FT sig_peptide 897. .218
FT CDS 897. .2138
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/mol_type="genomic DNA"
/db_xref="taxon:119602"
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1. .2568
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Pred. No. 2.3e-296;
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1 (bases 1 to 1401)
Hagenson,M.J. and Stroman,D.W.
Yeast production of streptokinase
Patent: EP 0248227-A1 5 09-DEC-1987;
Location/Qualifiers
1. .1401
GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA
                     GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCCAAGGCTTAAGTCCAAAAATCA
                                                                                           AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATC
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/mol_type="unassigned
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Pred. No. 1.1e-295;
0; Mismatches 10;
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                                                                                                                                     GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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Reed,G.L.
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Patent: US 5854049-A 19 29-DEC-1998;
Location/Qualifiers
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              CTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGA 1306
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/mol_type="unassigned
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Pred. No. 7.1e-294;
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SEQ ID NO: 35; Synthetic nucleotide sequence
Hirudin-streptokinase fusion protein.
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PATENT: WO 9109125-A 35 27-JUN-1991;
Cocation/Qualifiers
1. 1458
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synthetic construct
other sequences; artificial
1 (bases 1 to 1458)
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                                                                                                                                                           GCTGACTTACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGAC
                                                                                                                                CAATTGGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAA
                                                  AGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAA
                                                                                        TTTTTTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTA
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  GCTGACTTACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGAC
                                        AGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGCCACATAAACTTGAAAAA
                                                                              TTTTTTGAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTA
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Pred. No. 5.2e-292;
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Best Loc Matches

Local

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Score 1124.6; DB 1 Pred. No. 8.5e-292; 0; Mismatches 19;

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Query Match

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KEYWORDS
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ORGANISM
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                              /translation="IAGPEWILLDRPSVNNSQLVVSVAGTVEGTNQDISLKFFEIDLTS RPAHGCKTEQGLSPKSKFFEIDLTSKFFEIDLTSKFFEIDLTSKFFEIDGKSFKSKFFATDSGAMFHKLEKADLLKAIQEQLANVHSNDDYEVID FASDATITDMKKKVYFADKOGSVTLFTQPVDGEFLSGHTVURPYKEKTIQNQAKSVDV EYTVQFTFLNPDDDFRPGLKDTKLLKTLAIGDTITSQELLAQAQSILNKTHPGYTIYE EDSSIVHDNDIFRTILPMDQEFTYHVGNREQAYEINKKSGLLAFABLDFRDLYDRDKYAK EDSSIVHDNDIFRTILPMDQEFTYHVGNREQAYEINKKSGLLAFABLDFRDLYDRDKYAK LTANLDAFGIMDYTLTGKVEDNHDDTNRITITVYMGKRPEGENASYHLAYDKDRYTEB
                EREVYSYLRYTGTPIPDNPNDK"
                                                                                                                                                       /protein_id="AAC60418.1"
/db_xref="GI:257197"
                                                                                                                                                                                                          /note="streptokinase; Mature
/codon_start=1
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Vector for the production of transplastomic angiosperm Patent: WO 2004039256-A 26 08-APR-2004;
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Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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     TGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAA
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ADLIKAIQEQLI ANVHSNDDYFEVI DFASDATI TDRNGKVYFADKDGSVTLPTQPVQE FLLSGHVRVRPYKEKP IQNQAKSVDVEYTVQCTPLNPDDDFRECKDYKLLKTILAIGD TITSQELLAQAQSI INKTHPGYTI YERDSYTVQETTI LPENDEFTYHVKNREQ AYE INKKSGLNEEINNTDLI SEKYYVLKKGEKPYDPFDRSHLKLFTI KYVDVNTNELL KSEQLLTASERNILDFRDLYDFRDKAKLLYNNLDAFGINDYTLTGKVEDNHDDTNRI IT VYMGKRPEGENASYHLAYDKDRYTEEEREVYSYLRYTGTPI PDNPNDK"

CATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGA GAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAAGG GGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAA CAAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTTGCTAAGCGGACA AAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGT AAAACCATTTGCTACTGATAGTGGCGCGCATACTAAACTTGAAAAAGCTGACTTACT TGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCCAAGGCTTAAGTCCAAAATC TAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAAT TATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGT GAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAAGG GTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCT CTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGA CTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGA AGCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGA AGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACT AGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACT GGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAA TGTGCGCGTTAGACCATATAAAGAAAACCAATACAAAATCAAGCGAAATCTGTTGATGT TGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGT CAAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTTGCTAAGCGGACA AAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGT AAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACT CGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCCAAGGCTTAAGTCCAAAATC TATTGCTGGACCTGACTGCTAGACCGTCCATCTGTCAACAACAGCCAATTAGTTGT AGCTCAAGCACAAAGCATTTTAAACAAAACCCATCCAGGCTATACGATTTATGAACGTGA Conservative 53.5**%**; 98.2**%**; Score 1122.4; Pred. No. 3.4e 0; Mismatches 1122.4; DB 6; No. 3.4e-291; 21; Indels Length 0; Gaps 1426 1306 1246 1186 1126 1066 1006 1486 923 1366 803 623 563 503 443 946 383 886 323 826 203 143 646 863 743 683 263 766 706 983 0

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Dawson, K., Hunter, M.G. and Czaplewski, L.G.

Fibrinolytic and anti-thrombotic cleavable

Patent: US 5434073-A 14 18-JUL-1995;
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                     CAAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGAATTTTTGCTAAGCGGACA
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  TGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGT
                                                                                      CATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGA 946
                                                                                                                          AAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACTACTTTGAGGT
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/mol_type="unassigned
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SEQ ID NO: 24
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other sequences; artificial
1 (bases 1 to 1512)
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Patent: WO 9109125-A 24 27-JUN-1991;
Location/Qualifiers
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                                                                                                                  GAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATG
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                                                                                         GAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATG
                                                                                                                                                                              GAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAACCCATCCAGGCTATACGATTTAT
                                                                                                                                                                                                                         GAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTAT 1238
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/product="streptokinase fused to yeast alpha-factor"
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/db xref="G1:1247851"
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QAYEINKKSGLNEEINNTDLISEKYYVLKKGEKPYDPPDRSHLKLFTIKYVDVNTNEL
LKSEGLLTAASERNLDFRDLYDPRDKAKLLYNNLDAFGIMDYTLTGKVEDNHDDTNRII
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Pred. No. 3.4e-291;
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δ	1419	AAAAAAGGGGAAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATC 1478
Дb	1093	AAAAAAGGGAAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATC 1152
δ	1479	AAATACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGC 1538
Db	1153	AAATACGTTGATGTCAACACCAACGAATTGCTAAAAAAGCGAGCAGCTCTTAACAGCTAGC 1212
γ	1539	GAACGTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTAC 1598
Ъ	1213	GAACGTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAAGGCTAAACTACTCTAC 1272
δ	1599	AACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAAT 1658
рь	1273	AACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAAGATAAT 1332
γQ	1659	CACGATGACACCAACCGTATCATAACCGTTTTATATGGGCAAGCGACCCGAAGGAGAAAT 1718
DЪ	1333	CACGATGACACCCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAAT 1392
Qy	1719	GCTAGCTACCATTTAGCTGGTGGT 1742

Search completed: February Job time : 10656.6 secs 1, 2006, 04:17:49 문

1393

GCTAGCTATCATTTAGCCTATGAT

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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Quary Match Length	DB	ID	Description
1	2096	100.0	2096	ω	AAA37643	Aaa37643 Chimeric
2	1684	80.3	1782	w	AAA37642	
ω	1496.2	71.4	1541	w	AAA37644	
4	1165.8		1661	ω	AAA37637	-
S	1150.8		2385	N	AAX80497	-
0	1147	54.7	1377	w	AAA37622	
7	1145.4		1242	N	AAX80492	Aax80492 Streptoco
8	1145.4	54.6	1245	w	AAA37633	Aaa37633 S. equisi
9	1145.4		1254	σ	ABA05546	Aba05546 Streptoki
10	1145.4	54.6	8893	σ	ABA05547	Aba05547 Maxadilan
11	1143.8	54.6	1242	N	AAX16632	Aax16632 Streptoco
12	1143.8	54.6	2030	N	AAQ11651	Aaq11651 FB-FB-SK
13	1140.6	54.4	1242	N	AAX16633	Aax16633 Streptoco
14	1134.2		1327	ω	AAA37628	Aaa37628 Streptoki
15	1132.4	54.0	2566	N	AAT77778	Aat77778 Coding se
16	1125.4	53.7	1458	N	AAQ12162	Aaq12162 Factor Xa
17	1124.6	53.7	7057	12	ADM01294	Adm01294 Plasmid p
18	1122.4	53.5	1335	N	AAQ12156	
19	1122.4	53.5	1512	2	AAQ12158	Aaq12158 Streptoki

## ALIGNMENTS

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RESULT 1
AAA37643
ID AAA3
                                                                                              AAA37643 standard; DNA; 2096 BP
Chimeric SK-FBD coding sequence.
                            15-SEP-2003
13-OCT-2000
                                                                    AAA37643;
                           (revised)
(first entry)
```

Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy; cardiovascular disorder; ss.

Streptococcus dysgalactiae subsp. equisimilis. Chimeric.

EP1024192-A2

02-AUG-2000

23-DEC-1999; 99EP-00310541

24-DEC-1998; 98IN-DE003825.

(COUL ) CSIR COUNCIL SCI IND RES

Sahni G, Yadav M; Kumar R, Roy C, Rajogopal K, Nihalani D, Sundaram V;

WPI; 2000-516032/47.

Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.

Example 6; Fig 22b; 58pp; English.

This sequence represents a chimeric streptkinase-fibrin binding domain (SK-FBD) protein coding sequence. The invention relates to a hybrid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC plasminogen activator (PA) comprises a polypeptide fusion between CC fibrin binding regions of human fibronectin, which are from fibrin CC binding domains (PB) 4 and 5 or 1 and 2. The hybrid PA possesses the CC ability to bind with fibrin independently and also characteristically CC retains a PG activation ability which becomes evident only after a CC pronounced duration, or lag, after exposure of the PA to a suitable CC animal or human PC. The hybrid streptokinase-fibrin binding domain CC polypeptides are useful in thrombolytic therapy for various kinds of CC cardiovascular disorders. The hybrids have enhanced fibrin selectivity as CC well as kinetics of plasminogen activation that are distinct from that of CC natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of CC plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins CC can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating CC plasminogen to plasmin openess to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                     CTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTATTGCTGGACCTG
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This sequence represents a chimeric streptkinase-fibrin binding domain (SK-FBD) protein coding sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, fibrin binding regions of human fibronectin, which are from fibrin binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of
                                                                                                                                                                                                                                                                                                                                                                                                    Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin by domains of human fibronectin.
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Best Local Simi
Matches 1687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating plasminogen to plasmin, thus aiding in the localisation of the plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation nencountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
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                                            CCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTAAAG
                                                           CCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTAAAG
                                                                                                          CTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCAAAA
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99.7%;
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13-OCT-2000
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Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy; cardiovascular disorder; ss.
                                                                                                                                                                              Streptococcus
                                                                                                                                                                        Chimeric
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                                                                                                                                                                              dysgalactiae subsp. equisimilis
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02-AUG-2000

EP1024192-A2

23-DEC-1999; 99EP-00310541.

24-DEC-1998; 98IN-DE003825

(COUL ) CSIR COUNCIL SCI IND RES.

Kumar R, Ç Rajogopal ζ, Nihalani à Sundaram ۲,

WPI; 2000-516032/47

Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding human fibronectin.

Disclosure; Fig 17b; 58pp; English

This sequence represents a chimeric streptkinase-fibrin binding domain (SK-FBD) protein coding sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between contribution between the streptokinase (SK), which are capable of plasminogen (PG) activation, and contribution binding regions of human fibronectin, which are from fibrin contribution binding regions of human fibronectin, which are from fibrin contribution binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the contribution between the protein ability to binding domains (PBD) 4 and 5 or 1 and 2. The hybrid PA possesses the contribution and the protein activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable contribution of the proteins are useful in thrombolytic therapy for various kinds of contribution of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of contribution to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)

Sequence 1541 BP; 497 A; 328 C; 335 G; 381 T; 0 U; 0 Other;

DB 3;

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              AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA
                                                  GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA
                                                                GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCCAAGGCCTTAAGTCCAAAAATCA
                                                                                                     AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATC
                                                                                                                                                      ATAGCTGGTCCTGAATGGCTACTAGATCGTCCTTCTGTAAATAACAGCCAATTGGTTGTT
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                                                                                                                                                                                                      Conservative
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99.5%;
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0; Mismatches
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Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.

5 Fig 19b; 58pp; English.

binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolyvic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of This sequence represents a chimeric streptkinase-fibrin binding domain (SK-FBB) protein coding sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptckinase (SK), which are capable of plasminogen (PC) activation, a fibrin binding regions of human fibronectin, which are from fibrin that the first plasminogen (PC) activation. plasminogen to plasmin (i.e. delayed-action thrombolysis). The and

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The present invention describes an isolated bacterial protein that CC induces fibrin-dependent plasminogen activation in a pharmaceutical CC composition for dissolving blood clots. Also described are: (1) a CC composition comprising an isolated modified streptokinase, the CC composition comprising an isolated modified streptokinase, the CC modification being removal of amino acid residues in the amino terminus; CC (2) a method for dissolving a blood clot in a subject, comprising CC administering to the subject a fibrin-dependent streptokinase protein; a CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an CC expression vector comprising (1); and (4) a host cell transformed with CC the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving CC bacterial fibrin-dependent plasminogen activator is useful for dissolving conformation, venous thrombosis, pulmonary embolism, cerebral thrombosis, CC graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of
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AAA37622;

15-SEP-2003 13-OCT-2000 (revised) (first en entry)

Streptokinase-NTRN gene.

plasminogen; human; fibronect cardiovascular disorder; ss. SK; hybrid plasminogen activator; fibrin binding region; fibronectin; thrombolytic therapy;

Streptococcus dysgalactiae subsp. equisimilis

02-AUG-2000.

23-DEC-1999; 99EP-00310541

24-DEC-1998; 98IN-DE003825

(COUL ) CSIR COUNCIL SCI IND

Yadav Sahni `≅ ໌ບ Kumar R, Roy ú Rajogopal , ,× Nihalani 'n Sundaram <

WPI; 2000-516032/47.

Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin domains of human fibronectin. for rin binding

Example 1; Fig 11; 58pp; English

RESULT 6
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XX This sequence represents a streptokinase-NTRN (SK-NTRN) gene (where NTRN stands for N-terminally repaired with native sequence). The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, and fibrin binding regions of human fibronectin, which are from fibrin binding domains (PBD) 4 and 5 or 1 and 2. The hybrid PA possesses the ability to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that

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N-terminally deleted streptokinase

Claim 44; Page 58-60; 73pp; English.

induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an increase of the comprising (1) and (1) a host all transformed with expression vector comprising (I); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial The present invention describes an isolated bacterial protein that

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This sequence represents the human Streptococcus equisimilus streptokinase coding sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are capable of plasminogen (PG) activat:

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    equisimilis streptokinase

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CC fibrin binding regions of human fibronectin, which are from fibrin CC binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the CC ability to bind with fibrin independently and also characteristically CC retains a PG activation ability which becomes evident only after a CC pronounced duration, or lag, after exposure of the PA to a suitable CC animal or human PG. The hybrid streptokinase-fibrin binding domain CC polypeptides are useful in thrombolytic therapy for various kinds of CC well as kinetics of plasminogen activation that are distinct from that of CC matural streptokinase in being characterised by a temporary delay, or lag CC of several minutes in the natural rate of the catalytic conversion of CC plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins CC can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating CC blood plasminogen to plasmin, thus aiding in the localisation of the plasminogen activation encountered during clinical use CC overcomes systemic plasminogen activation encountered during clinical use CC of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
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                         TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 1307
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TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
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The invention relates to a fusion protein or a conjugate comprising vasodilator polypeptide, or its active fragment, and a thrombolytic polypeptide or its active fragment. The protein is useful for treating the protein is useful for treating the protein in the protein is useful for treating the protein in the protein is useful for treating the protein in the protein is useful for treating the protein in the protein is useful for treating the protein in the protein is useful for the protein in the protein in the protein is useful for the protein in the protein in the protein is useful for the protein in the protein in the protein is useful for the protein in the protein in

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1254 BP; 426 A; 271 C; 241 G;
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                                                                                                                                                                                                                                                                                                                                  GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 1187
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                                                                                                           TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG
                                                                                                                                                                                           TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
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The invention relates to a fusion protein or a conjugate comprising vasodilator polypeptide, or its active fragment, and a thrombolytic polypeptide or its active fragment. The protein is useful for treatily polypeptide or its active fragment. The protein is useful for treatily polypeptide or its active fragment. The protein is useful for treatily occluded blood vessel, and the protein its protein from a partially or totally occluded blood vessel.

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                                                                                                                                                                                                                                                                                           Streptokinase; vasodilator; th gene therapy; m
                                                                                                                                                                                                                                     WO200185100-A2
                                                                                                                                                                                                                                                            Lutzomyia longipalpis. Unidentified. Synthetic.
                                                                                                                                                                                                                                                                                                                             Maxadilan-streptokinase
                                                                                                                                                                                  11-MAY-2000; 2000US-00569920
                                                                                                                                                                                                   10-MAY-2001;
                                                                                                                                                                                                                   15-NOV-2001
                                                                                                                                                                                                                                                     Chimeric.
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                                                                                                                                                                                                                                                                                           e; cerebroprotective; cardiant;
thrombolytic; angina; myocardia;
; maxadilan; sand fly; plasmid;
                                                                                                                                                                                                   2001WO-US015209
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al infarction;
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GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
                                        GAAAAGCCGTATGATCCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
                                                                    GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 1487
                                                                                                                                                                     AATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG
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      The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence encodes native SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPIg) to plasmin (HPIm), which is a serine protease able to catalyse the hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                               plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; serine protease; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction; fibrinolysis; resistance; ds.
                                                                                                                     Mutant streptokinase thrombolytic agent.
                                                                                                                                                     WPI; 1999-189643/16.
P-PSDB; AAW94664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen. (Updated on 17-OCT-2003 to standardise OS field)
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larity 99.4%;
Conservative
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Pred. No. 0;
0; Mismatches
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                                       The DNA encodes an FB-FB dimer linked to the streptokinase coding sequence. The FB fragment has selective affinity for fibrin, low affinity for fibrinogen, and minimal immunogenicity, imparting thrombus-targetting capability. See also AAQ11649 and AAQ11650
                                                                                                                                                                                                                                                                         WPI; 1991-140198/19.
P-PSDB; AAR11829.
                                                                                                                                                         Disclosure; Fig 5; 18pp; English.
                                                                                                                                                                                                                        Imparting
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                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-1987;
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                                                                                                                                                                                                   injectable fibrinolytic agent - with affinity for by linking agent to fibrin binding domain.
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fusion protein; ss.
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Query Match

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Query Match 54.4 Best Local Similarity 99.3 Matches 1146; Conservative

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                                             The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the ProS8-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence encodes mutant SK K59E. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPlg) to plasmin (HPlm), which is a serine protease able to actalyse the hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with will-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen
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                                                  This sequence represents a streptokinase-NTR (SK-NTR) gene (where NTR CC stands for N-terminally repaired with native sequence). The invention CC relates to a hybrid plasminogen activator (PA) comprises a polypeptide CC fusion between streptokinase (SK), which are capable of plasminogen (PG) activation, and fibrin binding regions of human fibronectin, which are CC from fibrin binding domains (PB) 4 and 5 or 1 and 2. The hybrid PA CC possesses the ability to bind with fibrin independently and also CC characteristically retains a PG activation ability which becomes evident CC only after a pronounced duration, or lag, after exposure of the PA to a Suitable animal or human PG. The hybrid streptokinase-fibrin binding CC domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that CC of natural streptokinase in being characterised by a temporary delay, or CC lag of several minutes in the natural rate of the catalytic conversion of CC plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins CC an bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating CC overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 15-SEP-2003 to standardise OS field)
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GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                               TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 1607
                                                                                                                             GATGTCGATACCAACGAATTGCTAAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
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                                                                                                          GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC
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Best Local Similarity
Matches 1148; Conserv
                                                                                                                                                                                                                                                   This sequence encodes the wild type plasminogen-binding fragment of streptokinase. The protein fragment encoded by this sequence was used in the design of a modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, opt. as a bolus rather than by continuous infusion. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                           Modified forms of streptokinase resistant to enzymatic cleavage - usefu as thrombolytic agents in treating thrombosis and in medical equipment.
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01-OCT-1997
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Sequence 1, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 5, Appli	Sequence 9, Appli	Sequence 11, Appl	Sequence 15, Appl		Patent No. 5455158	Sequence 16, Appl	16, 1	Sequence 135, App	Sequence 1, Appli	1,	Sequence 6, Appli	Sequence 1289, Ap	Sequence 38, Appl	Sequence 13, Appl	Patent No. 5240845	55	Sequence 3, Appli

## ; LOCATION: US-09-211-542A-1 ; Sequence 1, Application US/09211542A ; Patent No. 6210667 NAME: Attorney, Stringel, Har: REGISTRATION NUMBER: 37,008 REFERENCE/DOCKET NUMBER: 1874, TELECOMMUNICATION: INFORMATION: TELEPHONE: (617)443-9292 TELEPHONE: (617)443-0004 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2385 base pairs TYPE: mucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/211,54 FILING DATE: 15-December-1998 CLASSIFICATION: 1653 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/069,497 FILING DATE: 15-December-1997 ATTORNEY/AGENT INFORMATION: GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk APPLICANT: Reed, Guy L. TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR NUMBER OF SEQUENCES: 14 FEATURE: CORRESPONDENCE ADDRESS: STREET: 125 SUCITY: Boston STATE: Massacl COUNTRY: USA COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 NAME/KEY: ADDRESSEE: Massachusetts E: BROMBERG & SUNSTEIN, LLP 125 Summer Street 1..2385 US/09/211,542A 1874/111 Harriet M.

Query Match

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                                                                                                                 ACCATCAAATACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACA
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FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Strimpel, Harriet
REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)443-9292
TELEFAX: (617)443-0004
INFORMATION FOR SEQ ID NO: 5:
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Best Local S
Matches 1149
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PATERIX NO. 6210667
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-Dece
CLASSIFICATION: 1653
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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FILING DATE: 15-December-1998
                                                                                                                                                                                                                                                                                                         NAME/KEY:
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Pred. No. 0;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1242 base pairs
TYPE: Nucleic Acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 1148; Conserv
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NAME: Chi-Ping Chang
REGISTRATION UNMER: 37,798
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 288-8585
TELEFAX: (408) 288-8386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hua-Lin Wu
APPLICANT: Guey-Yueh Shi
TITLE OF INVENTION: mutants as i
NUMBER OF SEQUENCES: 2
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ORIGINAL SOURCE:
ORGANISM: Streptococcus equisimilis H46A
INDIVIDUAL ISOLATE: Malke, H., Roe, B., and Ferretti, J. J.;
INDIVIDUAL ISOLATE: "Nucleotide sequence of the streptokinase gene from Strepto
INDIVIDUAL ISOLATE: equisimilis H46A" from Gene 34:357-362 (1985).
CELL TYPE: Streptococcus equisimilis H46A
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MEDIUM TYPE: Diskette, 3.50 inch
MEDIUM TYPE: Storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 on Wir
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ADDRESSEE: Jeing & Chang
STREET: Two No. 5876999th
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CLASSIFICATION: 435
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Pred. No. 0;
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                                                                                                               Sequence 2, Application Patent No. 5876999 GENERAL INFORMATION:
                                          APPLICANT: Hua-Lin nu
APPLICANT: Guey-Yueh Shi
TITLE OF INVENTION: Preparation
TITLE OF INVENTION: mutants as i
                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE:
STREET: Tw
CITY: San
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Matches 1146; Conserva
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INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 1242 base pairs
TYPE: Nucleic Acid
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COUNTRY: USA
ZIP: 95113
ZIP: 95113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
MEDIUM TYPE: storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: WordPerfect 6.1 on Window
CURRENT APPLICATION DATA:
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NAME: Chi-Ping Chang
REGISTRATION NUMBER: 37,
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LOCATION: DNA sequence No. 5876999174 and 175
LOCATION: from AA to GG, and PROTEIN sequence
LOCATION: from Lys to Glu.
OTHER INFORMATION:
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                                                                                                                                                                                                       Sequence 19, Application Patent No. 5854049
GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                             APPLICANT: Reed, Guy L
TITLE OF INVENTION: PLI
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                         ADDRESSEE: Fi
STREET: 225 F
CITY: Boston
STATE: MA
COUNTRY: USA
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; MOLECULE TYPE: US-08-488-940-19
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INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 2566 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity
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REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
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RESULT 6
US-07-854-596B-42
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                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILLNG DATE: 03-UN-1992
CLASSIFICATION: 435
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                                                                                                       TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1458 base pair
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic
                                              MOLECULE TYPE:
                                                                                                                                                                                     REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
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NAME: McDonnell, John J
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
CITY: Ch
STATE: I
COUNTRY:
ZIP: 606
                                                                        LENGTH: 1458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
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                                                                              AAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTC
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                                                                                                                           ATGGATCAAGAGTTTACTTACCATGTCAAAAATCGGGAACAAGCTTATGAGATCAATAAA
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                                                             AAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTC
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fusion linked by Factor Xa cleavable IEGR"
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                                                                                                                                                                                                                                       NAME: Michaelson, Peter L.
REGISTRATION NUMBER: 30090
REFERENCE/DOCKET NUMBER: Cent
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 530-6671
TELEPAX: (908) 530-6584
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07703778D Patent No. 5296366
GENERAL INFORMATION:
          ORGANISM: Streptococcus equisimiliorganism: definition
ORGANISM: definition
IMMEDIATE SOURCE: ATCC-9542 strain
PEATURE: from 1 to 1245 bp mature peromer information:
OTHER INFORMATION: Properties: Strain
OTHER INFORMATION: The gene product
OTHER INFORMATION: The gene product
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1245 base pairs
TYPE: NUCLEOTIDE WITH CORRESPONDING
                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2 Model 80
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/703,778D
FILING DATE: 19910522
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSE: Stanger, Michaelson, Spivak and Wallace,
STREET: Parkway 109 Office Center, 328 Newman Spring
STREET: P. O. Box 8489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GARCIA, M.P.E. et al TITLE OF INVENTION: METHOD FOR THE ISOLATION AND EXPRESSION TITLE OF INVENTION: METHOD FOR THE ISOLATION AND EXPRESSION TITLE OF INVENTION: OF A GENE WHICH CODES FOR STREPTOKINASE, NUCLEOTIDE SEQUENCE TITLE OF INVENTION: OBTAINED, RECOMBINANT DNA AND TRANSFORMED MICROORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 3 1/2" 1.44Mb IBM compatible
                                                                                                                                 MOLECULE TYPE: 9
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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STREET: P.
CITY: Red I
CITY: New
COUNTRY: US
ZIP: 07701
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          Properties: Streptokinase gene
The gene product binds to human plasminogen
The gene product is an activator of human p
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                                                                                                  GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1547
                                                                                                                                               GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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                                                                                             GCTCAAGCACAAAGCATTTTAAACAAAACCCACCCAGGCTATACGATTTATGAACGTGAC
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Qy 587 TATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGT 646	Query Match 53.5%; Score 1122.4; DB 2; Length 1335; Best Local Similarity 98.2%; Pred. No. 0; Matches 1135; Conservative 0; Mismatches 21; Indels 0; Gaps 0;	;		Į	FEATURE:  NAME/KEY: mis  LOCATION: 1	TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear MOLECULE TYPE: CDNA	TELEX: 910-221-5317 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 1335 base pairs	REFERENCE/DOCKET NUMBE TELECOMMUNICATION INFORM TELEPHONE: 312-715-1034 TELEPAX: 312-715-1234	CLASSIFICATION ATTORNEY/AGENT I NAME: McDonne REGISTRATION N	9	COMPUTER MEDIUM COMPUT OPERAT	CITY: Ch STATE: I COUNTRY: ZIP: 606	NUMBER OF SEQUENCES: 73 CORRESPONDENCE ADDRESS: Dr. John J. McDonnell STREET: Ten South Wacker Drive, Suite 3	APPLIC APPLIC APPLIC TITLE	שעוקו	Db 1141 CATTTAGCCTATGAT 1155	Oy 1728 CATTTAGCTGGTGGT 1742	CY 1000 ACCHAICAINACCGITTAINIGGGAAGCGACCCGAAGGAGAGAGTGCTAGCTAC 1727 Db 1081 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCGGAAGGAGAGAGTGCTAGCTA	1021 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC	Qy 1608 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1667
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GENERAL INFORMATION:
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Matches 1138;
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Best Local S
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 03-JUN-1992
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDOMMell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,3
TELECOMPUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIA Release #1.0, V
CURRENT APPLICATION DATA:
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LENGTH: 1512 base pairs
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
                                                                                                                                                                                                                                                                                                                  FEATURE:
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CITY: Chicago
STATE: IL
COUNTRY: USA
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LOCATION:
                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 7..1503
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OTHER INFORMATION: /not
OTHER INFORMATION: fust
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Ten South Wacker Drive,
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fused to a yeast alpha-factor"
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              Matches 1136;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UN-1992
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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LOCATION: 1..2589
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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       ATCAAAACCATTTGCTACTGATAGTGGCGCGATGCCACATAAACTTGAAAAAGCTGACTT
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by thrombin-cleavable VELQGVVPRG"
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; Sequence 25, Application U
; Patent No. 5434073
; GENERAL INFORMATION:
APPLICANT: Dawson, Kei
; APPLICANT: Hunter, Mic
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Best Local S
Matches 1134
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INFORMATION FOR SEQ ID NO:
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FEATURE:
NAME/KEY:
LOCATION:
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LENGTH: 1257 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPHAX: 312-715-1234
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NAME: McDonnell, John J
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/854,590
FILLING DATE: 03-JUN-1992
CLASSIFICATION: 435
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TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                           -854-596B-25
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: I
COUNTRY:
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OTHER INFORMATION: /notOTHER INFORMATION: fus:
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ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC 947
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                                                                                AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC 887
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Ten South Wacker Drive, Suite
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Proteins and nucleic acids
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Pred. No. 0;
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                                                           ; Sequence 18, Application US/07854596B
Patent No. 5434073
; GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nu.
NUMBER OF SEQUENCES: 73
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           CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive,
 STREET:
CITY: C
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Best Local Similarity
Matches 1134; Conserv
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
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FEATURE:
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COUNTRY: 60606
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OTHER INFORMATION: /notOTHER INFORMATION: str
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                       AAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
                                     AAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACAT
                                                                     ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC
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streptokinase gene"
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                                                                                                                                                                                                                                                                                                                                                                 Score 1121.4;
Pred. No. 0;
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                                                          STREET: Chicago
OPERATING SYSTEM:
                                                       COUNTRY:
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Sequence 46, Application US/07854596B Patent No. 5434073
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nuc.
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Su
                              ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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Best Local Similarity 98.2
Matches 1134; Conservative
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NAME/KEY:
LOCATION:
S-07-854-596B-46
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CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/07/854,
FILING DATE: 03-UN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: MCDORNELJ, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,31
TELECOMMUNICATION INPORMATION:
TELEPAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
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LOCATION:
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OTHER INFORMATION: /not OTHER INFORMATION: fus:
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              GAATATACTGTACAGTTTTACTCCCTTAAAACCCCTGATGACGATTTCAGACCAGGTCTCAAA 1127
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fusion linked by Factor Xa-cleavable IEGR"
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APPLICANT: Escalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14 re: 9
Patent No. 6309873
CURRENT APPLICATION NUMBER: US/09/374,038
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 14
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1100
                                                                    US-09-374-038-13
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US-09-374-038-13
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Query Match 52.2%;
Best Local Similarity 98.7%;
Matches 1102; Conservative
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                       LENGTH: 1122
TYPE: DNA
ORGANISM: Streptococcus equisimilis
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                                                                                                                                                                                                                                                                                                   Madrazo, Isis Del Carmen T. Garcia, Jose De Jesus De L. Ojalvo, Ariana Garcia Menendez, Alina Seralena Escalona, Elder Pupo
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                                                                                                                                                                                                                                    Sequence Listings 1-14 re:
Score 1093.6; DB 3
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0; Mismatches 14;
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CURRENT APPLICATION NUMBER: US/09/658,179; CURRENT FILING DATE: 2000-09-08; NUMBER OF SEQ ID NOS: 14; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 13; SEQ ID NO 13; LENGTH: 1122; TYPE: DNA; ORGANISM: Streptococcus equisimilis US-09-658-179-13
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APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Ojalvo, Ariana Garcia
APPLICANT: Menendez, Alina Seralena
APPLICANT: Mescalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14 re: 976
Patent No. 6413759
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 1102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
                GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCCATCACATCTCAAGAATTACTA
                                                                          GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
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ACCAACCGTATCATAACCGTTTATATGGGCAAGCGA 1703	GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1667 	TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 1607	GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1547	GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT 1487 	AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGG 1427 	TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 1367 	TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 1307	GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 1247
	67 83	07 23	47	87 3	27	67 3	07	47

Search completed: February 1, 2006, 12:43:44 Job time: 371.056 secs

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Result
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO8A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8A_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
    January 31, 2006, 17:06:30 ; Search time 1731.86 Seconds (without alignments) 10008.068 Million cell updates/sec
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US-09-940-235-10
US-09-940-235-5
US-09-940-235-6
US-09-940-235-6
US-09-940-235-6
US-10-474-792-657
US-09-940-235-3
US-10-120-49
US-10-216-120-49
US-10-941-601-70
US-10-741-601-70
US-10-741-600-238
US-10-741-600-238
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0	Sequence 246,	Sequence 78,	Sequence 245,	77	N	52			603	88,	654	654	Sequence 79,	22	12	Sequence 75,		Sequence 69,	Sequence 63,	Sequence 574	Sequence 38,
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## ALIGNMENTS

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APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Wahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: CHARACTERISTICS AND ALTERED PLASMINGGEN ACTIVATION
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT APPLICATION NUMBER: 09/471,349
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR APPLICATION NUMBER: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 2096
TYPE: DNA
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APPLICANT: Sahni, Girish
APPLICANT: Rojagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vapudha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, App. Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                             Best Local Sim Matches 2096;
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hybrid cassette
121 GGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGGCCAGGACCCCAACGCTGCCCG 180
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Pred. No. 0;
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Raja Niha Sund Sunda Yada NVENTI	GENERAL IN APPLICANT APPLICANT APPLICANT	RESULT 2 US-09-940-235-11 US-09-940-235-11 ; Sequence 11, Application US/09940235 · Publication No US200300599211	Oy 2041 ACACCTCTGTGCACACCACTCGACGGATCTGGCCCCTTCACCGATGTTGGTTAG 2096  Db 2041 ACACCTCTGTGCAGACCACTCGAGCGGATCTGGCCCCTTCACCGATGTTCGTTAG 2096	1981 GANANC TICCTICCAGTIGCATCTIGCA-CAGGCCAGGGAGAGTIGGAAGTGTGAGG	1921 ATCAGGACACAGGACATCCTATAGAATTGGAGGACACCTGGAGCAGAGGACAATTGGAGTAATTCGAG	1 GTACTTGCCTGGGAGAAGGCAGCGAACGCATCACTTCCACTTCTAGAATAGATGCAACG 	1 CTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGTAGATT	1741 GTGGCCAGGGGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGA	1681 TAACCGTTTATATGGGCAAGGGACCCGAAGGAGAATGCTAGCTA	1621 TTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGACCAACCGTATCA	OY 1561 ATTTATACGATCCTCGTGATAAGGCTAAAACTACTCTACAACAATCTCGATGCTTTTGGTA 1620	1501 ACGAATTGCTAAAAAGTGACCAGCTCTAACAGCTAACGAACG	р г	1381 ACAACACTGACCTGATCTCTGAGAATATTACGTCCTTAAAAAAGGGGAAAAGCGTATG 1381 ACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGGGAAAAGCCGTATG 1381 ACAACACTGACCTGATCTGTGAGAAATATTACGTCCTTAAAAAAAGGGGAAAAGCCGTATG	1321 ITANANAT COGGANCANGC ITA TANGAT CAN TANANAT C TOG IT TONA TANANATAN TANANATAN TANANATAN TANANATAN TANANATAN TANANATAN TANANAT COGGAN TANANAT COGGAN TANANAT COGGAN TANANAT COGGAN TANANAT COGGAN TANANAT COGGAN TANANATAN TANANAT COGGAN TANANAT COGGAN TANANAT COGGAN TANANATAN TANANAT COGGAN TANANAT COGGA	1261 CTCATGACAATGTCCGTACGATTTTACCAATGGATCAAGAGTTTACTTAC	Db 1201 GCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGACTCCTCAATCGTCA 1260 Ov 1261 CTCATGACAATGACATTTTCCGTACGGTTACGATCGATGAATGA

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FILE OF INVENTION: CHARACTERISTICS AND A PITTLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CCURRENT APPLICATION NUMBER: US/09/940,235
CCURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1782
TYPE: DNA
ORGANIGM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hybrid cassette
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CCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTAAAG
                                                      CTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCAAAA
                                                                                                        GTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATCGAT
                                                                                                                                                            GCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTTAGC
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; Sequence 9, Application US/09940235
; Publication No. US20030059921A1
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APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Cammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
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ITILE OF INVENTION: PROTEIN
ITILE OF INVENTION NUMBER: US/09/940,235
CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: NJ 3825/DEL/98
PRIOR FILLING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
Matches 1501; Conserv
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ORGANISM: Artificial
FEATURE:
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RESULT 4

US-09-940-235-10

Sequence 10, Application US/09940235

Publication No. US20030059921A1

GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajeopal, Kammara
APPLICANT: Nihalani, Deepak
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APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
ITITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
ITITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINGEN ACTIVATION
ITITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINGEN ACTIVATION
ITITLE OF INVENTION: PROTEIN
ITITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SA
ITITLE OF INVENTION: PROTEIN
ITITLE OF INVENTION NUMBER: US/09/940,235
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 4.0
ELNGTH: 1661
TYPOR: DAN
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Best Local Similarity
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ORCANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Hybrid cassette
-09-940-235-10
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                                                          GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
                                                                                                                               GATACTAAGCTATTGAAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
                                                                                                                                                                            GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA
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                                                                                                      GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
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Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 5
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                                                                                                                                                                                ; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
US-09-940-235-5
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US-09-940-235-5
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GENERAL INFORMATION:

APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Rojagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINGEN ACTIVATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
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TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
                                                                                    Query Match 54.7%;
Best Local Similarity 99.6%;
Matches 1150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09940235 Publication No. US20030059921A1
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ATTGCTGGACCTGAGTGGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT
                       ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACACACCCAATTGGTTGTT
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                                                                                    Score 1147; D
Pred. No. 0;
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APPLICANT: NAME OF INVESTIGATION OF SAID

APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yaddav, Mahavir
ITILE OF INVENTION: NOVEL CLOT-SPECIFIC STREETOKINASE
ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
ITILE OF INVENTION: PROTEIN PROTEINS
FILE OF INVENTION: PROTEIN
FILE OF INVENTION: PROTEIN
FILE REFERENCE: 07664-009902
CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT APPLICATION NUMBER: 09/471,349
PRIOR APPLICATION NUMBER: 199912-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Streptococcus e
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1242)
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APPLICANT: Sahni Girish
APPLICANT: Roy, Chait
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Sequence 6, Application US/09940235

Publication No. US20030059921A1

GENERAL INFORMATION:

APPLICANT: Kumar, Rajesh
APPLICANT: Kumar, Girish
APPLICANT: Kumar, Cirish
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
ITILE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
ITILE OF INVENTION: PROTEIN
CURRENT OF INVENTION: PROTEIN
CURRENT APPLICATION NUMBER: US/09/940,235

CURRENT APPLICATION NUMBER: US/09/940,235

PRIOR APPLICATION NUMBER: 09/471,349

PRIOR PILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
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; SOFTWARE: FastSEQ for Windows V
; SEQ ID NO 6
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Streptococcus equisi
US-09-940-235-6
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Best Local Similarity
Matches 1142; Conser
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Sequence 657, Application US/10474792

Publication No. US20040236072A1

GENERAL INFORMATION:
APPLICANT: Olmsted, Stephen
APPLICANT: Zagursky, Robert
APPLICANT: Mickbarg, Elliot
APPLICANT: Winter, Lourie
INTLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID MOS: 674
SOFTWARE: PatentIn version 3.0
SEQ ID NO 657
LENGTH: 1323
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Best Local Similarity 91.3
1056; Conservative
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ORGANISM: Streptococcus pyogenes
10-474-792-657
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                                                                                          CATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGA
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        CAAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGAATTTTTTGTTAAAGGGACA
                                                                        CATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGA
                                                                                                                                         AAAAGCTATTCAAAAACAGCTGATCGCTAACGTTCACAGTAACGACGGCTACTTTGAGGT
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Pred. No. 1.9e-277;
0; Mismatches 100;
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Sequence 3, Application US/09940235

Publication No. US20030059921A1

GENERAL INFORMATION:

APPLICANT: Kumar, Rajesh
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish

APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Yadav, Mahavir

TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE

TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION OF STITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION OF STREPTOKING PROTEIN PILE REPERENCE: 07064-009002

CURRENT APPLICATION NUMBER: US/09/940,235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49, Application US/10210120 Publication No. US20030175736A1 GENERAL INFORMATION:
                                                                                                                                                                                            SEQ ID NO 49
                                         Matches 330;
                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                      APPLICANT: Sreekumar, Arun
TITLE OF INVENTION: Expression Profile of Prostate Cancer
FILE REPERENCE: UM-0721
CURRENT APPLICATION NUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 330;
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Best Local Similarity
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PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION:
                                                                                                                                   TYPE: DNA
ORGANISM: Homo
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ORGANISM: Homo sapiens
FEATURE:
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                                     15.7%; Score 330; DB 6; ilarity 100.0%; Pred. No. 3.9e-84; Conservative 0; Mismatches 0;
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Publication No. US20050118625A1
; GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WIT
TITLE OF INVENTION: HUMAN OSTEOARTHRIT:S AND HUMAN PROTEASES
TILE OF INVENTION NUMBER: US/10/956,157
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4288
; LENCTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 330;
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                        AGCGGATCTGGCCCCTTCACCGATGTTCGT 2093
                                                                                                          ACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 206:
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AGCGGATCTGGCCCCTTCACCGATGTTCGT 926
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100.0%; Pred. No. 3.9e-84;
tive 0; Mismatches 0;
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; LENGTH: 2443
; TYPE: DNA
; ORGANISM: Homo s
US-10-741-601-70
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US-10-741-601-70
(S-10-741-601-70
; Sequence 70, Application US/10741601
; Publication No. US20040166519A1
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
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; ORGANISM: Homo
US-10-909-035-49
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US-10-909-035-49
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APPLICANT: Chinnaiyan, Arul M.

APPLICANT: Laxman, Bharathi

APPLICANT: Sreekumar, Arun

TITLE OF INVENTION: AMACR Cancer Markers

FILE REFERENCE: UM-09098

CURRENT APPLICATION NUMBER: US/10/909,035

CURRENT FILING DATE: 2004-07-30

NUMBER OF SEQ ID NOS: 123

SOFTWARE: Patentin version 3.2
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                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 70
Query Match 15.7%; Score 330; DB 7; Best Local Similarity 100.0%; Pred. No. 4.2e-84; Matches 330; Conservative 0; Mismatches 0;
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LENGTH: 2127
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens: US-10-741-600-238
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 238
LENGTH: 2443
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WESULT 15
US-10-741-601-75
US-10-741-601-75
Sequence 75, Application US/10741601
Publication No. US/20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
PILE REFERENCE: CL001500
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 75
LENGTH: 2488
TYPE: DNA
CORGANISM: Homo sapiens
US-10-741-601-75
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Search completed: February 1, 2006, 14:21:22 Job time : 1732.86 secs
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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| /cgm2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	Sequence 104, App Sequence 116, App Sequence 107, App Sequence 693, App	Sequence 111, App Sequence 111, App Sequence 113, App Sequence 108, App	6, Ap 3, Ap 114, 105,	Sequence 12, Appl Sequence 11, Appl Sequence 9, Appli Sequence 10, Appl Sequence 5, Appli Sequence 1, Appli	Description

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Sequence	Sequence I	Sequence	Sequence :	Sequence	Sequence	Sequence :	Sequence ·	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence '	Sequence	Sequence	sequence.
87, Appl	86, Appl	17, Appl	254, App	1, Appli	13237, A	33, Appl	43, Appl	1, Appli	8, Appli	1, Appli	67, Appl	14, Appl	13, Appl	18, Appl	17, Appl	15, Appl		72, Appl	72, Appl	416, App	416, App	440, AP

## ALIGNMENTS

RESULT 1 US-10-631-558-12

Sequence 12, Applica Publication No. US20 GENERAL INFORMATION:

Application US/10631558

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APPLICATI: Yadav, Mahavir

APPLICANT: Yadav, Mahavir

IITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE

IITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

IITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID

IITLE OF INVENTION: PROTEIN

IITLE OF INVENTION: PROTEIN

IITLE OF INVENTION NUMBER: US/10/631,558

CURRENT APPLICATION NUMBER: US/09/940,235

PRIOR PILING DATE: 2002-04-09

PRIOR PILING DATE: 2002-04-09

PRIOR PILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US/09/940,235

PRIOR RELIGATION NUMBER: 09/471,349

PRIOR PILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-12-23

SPAIOR FILING DATE: 1998-12-24

NUMBER OF SEQ ID NOS: 28

SOPTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Giris
APPLICANT: Roy, Chait
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                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Roy, Chait
Roy, Chait
Rajagopal, Kammara
Nihalani, Deepak
Sundaram, Vasudha
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RESULT 2  (S-0-631-558-11  (Sequence 11, Application US/10631558  (Publication No. US20050260598A1  (GENERAL INFORMATION:  (APPLICANT: Kumar, Rajesh  (APPLICANT: Sahni, Girish  (APPLICANT: Roy, Chait  (APPLICANT: Rajagopal, Kammara  (APPLICANT: Nihalani, Deepak  (APPLICANT: Sundaram, Vasudha	Db 1201 GCTTTTPAACAATGAAATGACATTTTACGATTTTACGATTGATTACAATGATTACTTAC	Qy 1201 GCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGACTCC

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APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1998-12-24
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1782
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CTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCAAAA
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                                                                                                                                                                                                                                    GACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGAT 1610
                                                                                                                                                                                                                                                                                                                                       AAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTTGAT 1490
                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAGGGGGAA 1430
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Sequence 9, Application US/10631558

Publication No. US20050260598A1

GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINGEN ACTIVATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
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CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PastSEQ for Windows Version 4.0
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LENGTH: 1541
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 99.5%;
Matches 1501; Conservative
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Pred. No. 0;
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Application US/10631558
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GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajegopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION OF SA
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SA
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-09002
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR APPLICATION NUMBER: 109/471,349
PRIOR APPLICATION NUMBER: 1N 3825/DEL/98
PRIOR APPLICATION NUMBER: 1N 3825/DEL/98
PRIOR APPLICATION DATE: 1998-12-24
NUMBER OF SEO ID NOS: 28
SOPTWARE: FastSeQ for Windows Version 4.0
SEQ ID NO 10
SEQ ID NO 10
LENGTH: 1661
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local
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OTHER INFORMATION: Hybrid cassette
-10-631-558-10
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Pred. No. 0;
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                CATTTAGCTGGTGGTGGCCAGGCCCAACAGATTGTAC 1764
                                                                        GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
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Sequence 5, Application US/10631558

Publication No. US20050280598A1

GENERAL INFORMATION:

APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaran, Vasudha
APPLICANT: Sundaran, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR PILING DATE: 1909-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR PILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOPTMARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1377

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; ORGANISM: Streptococcus equisimilis
US-10-631-558-5
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                   GATÁCTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTAAGAATTACTA 1187
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 TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 1607
                                                                                                                                    TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG
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8	ф	ş	DЬ	Ş	유 왕	Db 43	Query Best Match	; SEQ II TYP; ORG, FEAN; LOC. US-10-6								ro ta	Db	Ş	뮹	Q	₽ &	DЪ
828 AAGGCTATTCAAGAACAATTGATCGCTAACGTCACAGTAACGACGACTACTTTGAGGTC 887	181 AAACCATTTGCTACTGATAGTGGCGCGCATGTCACATAAACTTGAGAAAGCTGACTTACTA 240	768 AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTA 827	121 GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA 180	708 GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA 767	648 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAATC 707	1 ATTGCTGAACCTGAGTGGCTAGACCGTCCATCTGTCAACAACAGCCAATTAGTTGTT 60	54.6%; Score 1145.4; DB 7; Length 1245; Similarity 99.5%; Pred. No. 0; 9; Conservative 0; Mismatches 6; Indels 0; Gaps	5 Streptococcus equisimilis  DS  (1)(1242)	PRIOR APPLICATION NUMBER: IN 3825/DEL/98 PRIOR FILING DATE: 1998-12-24 NUMBER OF SEQ ID NOS: 28 SOFTWARE: FAStSEQ for Windows Version 4.0	OR APPLICATION NUMBER: US/09/940,235 OR FILING DATE: 2002-04-09 OR APPLICATION NUMBER: 09/471,349 OR FILING DATE: 1999-12-23	FILE REPERENCE: 07064-009002 CURRENT APPLICATION NUMBER: US/10/631,558 CURRENT FILING DATE: 2003-07-31	TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID TITLE OF INVENTION: PROTEIN	LICANT: Sundaram, Vasudha LICANT: Yadav, Mahavir LE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE	LICANT: Roy, Chait LICANT: Rajagopal, Kammara LICANT: Nihalani, Deepak	APPLICANT: Sahni, Girish	SULT 6 3-10-631-558-1 Sequence 1, Application US/10631558 Publication No. US20050260598A1 GENERAL THEORYMEN.	1273 CATTTAGCCTATGAT 1287	1728 CATTTAGCTGGTGGT 1742	1213 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAGA	1668 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAC 1727	1608 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1667 	TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC

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US-10-631-558-6
US-10-631-558-6
; Sequence 6, Application US/10631558
; Publication No. US/20050260598A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chait
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
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APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
ITILE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SA
TITLE OF INVENTION: PROTEIN
CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT APPLICATION NUMBER: US/9/940,235
PRIOR APPLICATION NUMBER: US/9/940,235
PRIOR APPLICATION NUMBER: US/9/940,235
PRIOR APPLICATION NUMBER: US/9/471,349
PRIOR APPLICATION NUMBER: US/9/471,349
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEG ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Streptococcus
US-10-631-558-6
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Best Local Similarity
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                                                      GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 1247
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APPLICANT: ROY, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
TILIE OF INVENTION: US/05/40,235
CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT APPLICATION NUMBER: US/09/40,235
PRIOR APPLICATION NUMBER: US/09/40,235
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR TILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-24
PRIOR FILING DATE: 1998-12-24
                              ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
US-10-631-558-3
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/1063158
Publication No. US20050260598A1
GENERAL INFORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
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                                                                                                                 SEQ ID NO 3
LENGTH: 777
 Query Match
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                     TYPE: DNA
ORGANISM: Homo
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TYPE: DNA
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Local Similarity 100.0%;
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GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/95,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 114
                                                                                                                                                                                                                                                                                                                                                                                                                                      1764 CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG
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ACAGGCAACGGCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG
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; Sequence 112, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METITILE OF INVENTION: DETECTION AND USES THEREOF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT FILING DATE: 2004-11-24
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 112
LENCTH: 6510
; TYPE: DNA
; ORGANISM: Homo sapiens
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Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION DETECTION AND USES THEREOF
TITLE OF INVENTION MIMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION SET 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NO 105
SEQ ID NO 105
LENGTH: 2488
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-995-561-112
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US-10-995-561-105
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Matches 330; Conserv
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CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 117
LENGTH: 7823
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-117
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US-10-995-561-117
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
                                                                                                                                                                                                                                                                                                                               Query Match

Best Local Similarity 100.0%; Pred. No. 1.7
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Best Local Similarity
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                             ACAGGCAACGGCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 2063
                                                                                         AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAAACCTGCTCCCAGTGCATCTGC
                                                                                                                                                                   GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT 1943
                                                                  AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
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100.0%; Pred. No. 1.5e-89;
                                                                                                                                                                                                                                                                                                                                       Score 330; DB 7; 1; Pred. No. 1.7e-89; 0; Mismatches 0;
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RESULT 14

US-10-995-561-113

Sequence 113, Application US/10995561

Publication No. US20050272054A1

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARTOIL, Michele et al.
APPLICANT: CNEUTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION UDIFECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 113

LENCTH: 7935

TYDE: DNA

ORGANISM: Homo sapiens
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION UNDHER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 111
SEQ ID NO 111
LENGTH: 7848
TYPE: DNA 6
ORGANISM: Homo sapiens
US-10-995-561-111
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US-10-995-561-111
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Publication No. US20050272054A1
GENERAL INFORMATION:
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Best Local
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100.0%;
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Pred. No. 1.7e-89;
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; Sequence 108, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF 52G ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 108
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; ORGANISM: Homo sapiens
US-10-995-561-108
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US-10-995-561-108
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Best Local Similarity
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ch completed: February 1, 2006, 14:43:15 time : 387.523 secs	2064 AGCGGATCTGGCCCCTTCACCGATGTTCGT 2093	

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Result
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## ALIGNMENTS

Query Match Best Local	ORIGIN	FEATURES BOUTCE	RESULT 1 AL603368 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT
Match 15.7%; Score 330; DB 1; Length 451; Local Similarity 100.0%; Pred. No. 8.4e-84;	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="pKrZp666C067" /dev_stage="adult" /lab_host="DH10B" /clone_lib="686 (synonym: hlcc3)" /note="Wector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"	Ingolataedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available. This clone (DKFZp686C067) is available at the RZPD in Berlin. This contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers 1. 451	AL603368  AL603368  DKFZp686C067 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686C067 5', mRNA sequence.  AL603368  AL603368.1 GI:15166874  EST.  Homo sapiens (human)  Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 451) Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.) Unpublished (1999) Contact: MIPS MIPS MIPS MIPS MIPS MIPS MIPS MIPS

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230 Constitution Drive,
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Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,
Lebkowski,J and Stanton,L.W.
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Length: 560 Std Error:
                                                                              /tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone_lib="GRN_EB" /note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p22), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
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/db_xref="taxon:9606"
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621 bp mRNA linear EST 26-APR-20 hw20d08.y1 Human primary human ocular pericytes. Unamplified (hw) Homo sapiens cDNA clone hw20d08 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                       Email: graeme@helix.nih.gov
Plate: 20 row: d column: 0!
Seq primer: M13RP1 reverse pi
Location/Qualifiers
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6/331, NIH, Bethesda, MD 20892-2740, USA
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/note-"organ: Eye; Vector: pSport1; RNA was extracted f primary human pericytes in culture. A directionally cle CDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in t manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGATCGCGGAGCGGCCCC(T)15-3']. cDNA was
                                                                                                                                                                                              /clone lib="Human primary human ocular pericytes.
Unamplified (hw)"
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/dev_stage="Adult"
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Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, J.
Lebkowski, J and Stanton, L.W.
                                                                                                                                                                              230 Constitution Drive, Menlo Park, Tel: 650 473 8658
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/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone_lib="GRN_BB" /clone_lib="GRN_BB" /note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free codition.
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                                                                                                                                                                                                                                                                                                                                                                   Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y. and Isogai,T. HRI human cDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU140993
AU140993
                                                                                                                                                                              Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                          Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
AU140993
                                                                                                                                                                                                                                                                                                                                                  Genomics Laboratory
                                                                                                                                                                                                                                                                            Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 737)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Location/Qualifiers
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                                /tissue_type="placenta"
/clone_lib="PLACE4"
                                                                   clone="PLACE4000626"
                                                                                    organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 9.3e-84;
             PME18SFL3"
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cDNA clone
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PLACE4000626 5', mRNA
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ACCESSION
VERSION
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AUTHORS
TITLE
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                                                                                                                                                                                                          Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                University of Iowa
375 Newton Road , 4156 MEBRP, Iowa City,
Tel: 319 335 8250
Pax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM715855
BM715855.1 GI:19029113
EST.
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UI-E-EJO-ahj-h-11-0-UI.r2 UI-E-EJO Homo sapiens cDNA
UI-E-EJO-ahj-h-11-0-UI 5', mRNA sequence.
                                                                                                                                                                                              Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                             Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                8889548
                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Mormalization and subtraction: two appr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                   /mol_type="mrurn
/db_xref="taxon:9606"
/dlome="UI-E-EJO-ahj-h-11-0-UI"
/tissue_type="fetal eyes, lens, eye /
/tissue_type="fetal, Retina Foveal a
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies)
                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="UI-E-EJO"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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KEYWORDS SOURCE RESULT 7 AU140971 COMMENT REFERENCE LOCUS DEFINITION VERSION ACCESSION JOURNAL. TITLE AUTHORS ORGANISM Hominidae; Homo.

1 (bases 1 to 861)

1 (bases 1 to 861)

1 (bases 1 to 861)

Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y. and Isogai, T., Nishikawa, T., Nakamura, Y., Suzuki, Y., Saito, K., Ishii, S., HRI human cDNA project (Ota, T., Suzuki, Y., Saito, K., Ishii, S., HRI human cDNA project (Ota, T., Suzuki, Y., Saito, K., Ishii, S., HRI human cDNA project (Ota, T., Nakamura, Y., Sugano, S., Yamamoto, J., Sugiyama, T., Masuho, Y., Isogai, T.) Unpublished (2000) Contact: Takao Isogai Genomics Laboratory Helix Research Institute AU140971 PLACE4 Homo Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens (human) 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan AU140971.1 GI:11002492 Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; 861 bp mRNA sapiens cDNA clone PLACE4000583 linear EST 05-AUG-2002

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RESULT 8
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
MCKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cranıata
Mammalia; Eutheria; Euarchontoglires;
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/mol_type="mRNA"
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/clone_lib="PLACE4"
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Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 168 Row: o Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 47132556
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2004) National Institutes of Health, Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Michael Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. Stefan Hansson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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ACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 2063
                                                                                                         AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC 2003
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/clone Tib="NIH MGC_147"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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n. Mismatches 0;
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CE 1 (bases 1 to 7501)

RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausmer, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusian, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D. K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                            Series: IRAK Plate: 198 Row: j Column: 21
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 4
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-AUG-2005) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                 Dickson, M.,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael Brownstein / Ted Usdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                        organism="Homo sapiens"
                                                                                                             Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
                             type="mRNA"
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Best Local Similarity
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                                                                                                                                              Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686K08164) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:

Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686K08164

Further information about the clone and the sequencing project is
                                                                                                                                                                                                                                                                                             Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Car
Research Center (OKPZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
                                                                                                          available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fobo,
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CR749316.1
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                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 7777)
Koehrer, K., Beyer, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.
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,G., Han,M. and Wiemann,S.
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/mol_type="mRNA"
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/clone_lib="NIH_MGC_147"
/lab_host="DH10B"
                                                              organism="Homo sapiens"
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Pred. No. 2.1e-83;
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tissue\_type="uterus endothel, primary cell culture"

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CHPVGTDEEPLQFRVPGTSTSATLTGLIRGATYNIIVEALKDQQRHKVREEVVTVGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDLKETQVTTTSLSAQWTPBNVQLTGYRVRVTPKEKTGPMKEINLAPDSSSVVVSGLM
VATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRRARVTDATETTITJSWRTKTETI
TGFQVUDAVPANGQTPIQRTIKEDVRSYTITGLQPGTDYKIYLYTLNDIMARSSPVVIDA
STAIDAPSNLRFLATTFNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRPRPGVTE
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QTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVTDSGVVYSVGMQWLKTQGNKQMLCT
CLGNGVSCQETAVTQTYGGNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNY
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GNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRPHET
GGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDNGVNYKI GEKWDRQGENGQMMSCTCLGNGKGEFKCD PHEATCYDDGKTYHVGEQWQ
KEYLGAI CSCTCFGGQRGWRCDNCRRPGGEPTPEGTTGQSYNQYSQRYHQRTNTNVNC
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DH10B; sites SfilA + SfilB"
/dev_stage="adulf"
/note="fibronectin 1, differentially spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNEGLNQPTDDSCFDPYTVSHYAVGDBWERMSESGFKLLCQCLGFGSGHFRCDSSRWC
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/product="hypothetical protein"
/protein id="CAH18171.1"
/protein id="CAH18171.1"
/db_xref="GI:51476362"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIECFMPLDVQADREDSRE"
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Pred. No. 2.1e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Canc
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology
Braunschweig/Germany) within the cDNA sequencing consortium o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    available at http://mips.gsf.de/projects/cdna/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone (DKFZp686M04163) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bloecker,H., Boecher,M., Brandt,P., Mewe
Osanger,A., Fobo,G., Han,M. and Wiemann,
The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686M04163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German Genome Project
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BX640608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="uterus endothel, /clone_Tib="886 (synonym: hlcc: DH10B; sites SfilA + SfilB" /dev_stage="adult" /note="fibronectin precursor"
                      GNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRPHET
GGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVVDCTCLGE
GSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCERHTSV
                                                                                       /db_xref="InterPro:IPR006209"
/db_xref="UniProt/TrEMBL:Q6N0A6"
/translation="MLRGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQGMVQPQSPVA
/translation="MLRGPGPGLLLLAVLCLCTGYGGSRGFNCESKPEAEETCFDKYT
VSQSKPGCYDNGKHYQINQQMBRTYLGNALVCTCYGGSRGFNCESKPEAEETCFDKYT
QTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVTDSGVVYSVGMQWLKTQGNKQMLCT
                                                                                                                                                                                         /db_xref="InterPro:IPR000083"
/db_xref="InterPro:IPR000562"
/db_xref="InterPro:IPR002086"
/db_xref="InterPro:IPR003961"
                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein id="CAB45714.1"
/db xref="GCB1:34364617"
/db_xref="GOA:Q6N0A6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="RZPD:DKFZp686M04163Q"
                                                                                                                                                                                                                                                                                                                                                                                             codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                 gene="DKFZp686M04163"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="DKFZp686M04163"
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Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .7868
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3). Vector pSport1_Sfi; host
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of the
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           987
                                      Homo sapiens mRNA; cDNA CR749281 CR749281.1 GI:51476291
Homo sapiens (human)
                                                                                                  CR749281
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT 1943
                                                                                                                                                                                               AGCGGATCTGGCCCCTTCACCGATGTTCGT 1136
                                                                                                                                                                                                                                                                                                                                                                           AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG
                                                                                                                                                                                                                                    AGCGGATCTGGCCCCTTCACCGATGTTCGT 2093
                                                                                                                                                                                                                                                                                                                ACAGGCAACGGCCGAGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG
                                                                                                                                                                                                                                                                                                                                                       AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGC
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NGKGEFKCDPHEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCRRPGG
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VSASDTVSGFRVEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRKYIVNVYQISEDGE
QSLILSTSQTTAPDAPDDPTVDQVDDTSIVVRWSRPQAPITGYRIVYSPSVEGSSTEL
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GTFYQIGDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFITETPSQPN
SHPIQWNAPQPSHISKYLLRWRPKNSVGRWKBATIPGHLNSYTIKGLKPGVVYEGQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLGNGVSCQETAVTQTYGGNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNY
EQDQXYSFCTDHTVLVQTRGGNSNGALCHPPFLYNNHNYTDCTSEGRRDNMKWCGTTQ
NYDADQKFGFCPMAAHEEICTTYNEGVMYKIGDQWDKQHDMGHMYRCTCVGNGRGEWTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPTPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQADREDSRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 330; DB 4;
; Pred. No. 2.1e-83;
0; Mismatches 0;
                                                                            7885 bp mRNA linear HTC 19-AUG-2004 DKFZp686F10164 (from clone DKFZp686F10164).
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ORIGIN

RESULT 12 CR749281

Pocas

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SOURCE

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FEATURES
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http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686F10164
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Research Center (DKFZ);
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1 (bases 1 to 7885)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koehrer, K., Beyer, A., Mewes, H.W., Pobo, G., Han, M. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDTWSKKDNRGNLLQCICTGNGRGEWKCERHTSVQTTSSGSGFFTDVRAÄVYQPQPHE

QPEPYGHCVTDSGVVYSVGMYMLKTQCRKQMLCTCLGRAVSCQETAVTQTYGGRSNGS

PCVLPFTYNGRTPYSCALTEGRODGHLMGSTTSRVEDQDKYSFCTDHTVLVQTRGGNSNG

GALCHFPFLYNNHNYTDCTSEGRRDNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNE

GYMYRIGDQWDKQHDMGHYMRCTCVGNGRGEWTCIAYSQLRDCCIVDDITYNNUDTFH

KRHEEGHMLACTCFGQGRGRMKCDPUDQCDDSETGTFYGIGBSWEKYHGVRYQCYCY

GRGIGEWHCQPLQTYPSSGPVEVFITETFSQPNSHFIGWNAPQPSHISKYILKWRPK

GRWHCQPLQTYPSSGPVEVFITETTSGQLISIQQHQBYTRFDFTTTSTSTPV

TSNTTVTGETTPFSPLVATSESVTEITASSFVVSWCASDTVGFRVETELSEGDEPQ

VLDLFSTATSVNIFDLLFGRKYIVNYQISEDGSGTFLNFETANSVTADAPDPTVDQV

DDTSIVVRGRRDAPITGYRIYSSPSEGSSTELNLFETANSVTADAPDFTCDGV

VDDTSIVVRGRRDAPITGYRIYSSPSEGSSTELNLFETANSVTADAPDFTCDGV

NOTSTATSVNIFTANSVTATAVARAPDFTVDQV

TSNTTVTGETTPRSPLATATSTATAVARAPDFTVDQV

TSNTTVTGETTPRSPLATATSTATAVARAPDFTVDQV

TSNTTVTGETTPRSPLATATSTATAVARAPDFTVDQV

TSNTTVTGETTPRSPLATATSTATAVARAPDFTVDQV

TSNTTVTGETTPRSPLATATSTATAVARAPDFTVDQV

TSNTTVTGETTPRSPLATATAVARAPDFTVDQV

TSNTTVTGETTPRACATAVARAPDFTVDQV

TSNTTVTGETTPRACATAV
                                                                                                                                                                                                                                                                                                                                       VAUEENQBSTPVVIQQETTGTPRSDTVPS PRDLQPTVBVTDVKTIMWTPPESAVTGYX
VDVIPVNLPGEHEQRLE I SRNTPAEVTGLS PGVTYYFKVAVSHGRESK PLTAQQTTK
LDAPTNLQPVNETDSTTVLVNWTPAEVTGLS PGVTYYFKVAVSHGRESK PLTAQQTTK
LDAPTNLQPVNETDSTTVLVNWTPPRAQITGKSLAVGLTRRGQPRQYNVGPSVSKY PLR
NLQPASEYTVSLVAI KGNQES PKATGVFTTLQPGSS I PPYNTEVTETTI VI TWTPAPR
IGFKLGVRPSQGGEAPREVTSGSGS I VPSGTTGYRT TTTPTNGQQGMADPI VNKV
VTPLS PPTNLHLEANPDTGVLTVSWERSTTDDTGYRT TTTPTNGQQGMADELEEVVHAD
OSSCTFDNLSPGLEYNVSVYTVKDDKESVPI SDTI I PAVPPPTDLRFTNI GEDTMRVT
                                                                                                           WAPPESIDLTNFLIRYSPVKNBEDVABLS ISPSDNAVVLTNLLDGTEYVVSVSSVYBQ
HESTPLRGRQKTGLDSPTGIDFSDITANSTWHIAPRATITGYRIRHPEHFSGRPR
EDRVPHSRNSITLTNLTPGTBYVVSIVALNGRBESPLLIGQQSTVSDVPRDLEVVABI
PTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDYTITV
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YLGARLVCTCYGGSRGENCESKPEAESTGDKYTGMTYRVGDTYSREPKDSMIWDCTCV
GAGRGRISCTIANRCHEGGGSYKIGDTWRRPHETTGGYMLECVCLLGNGKGEWTCKPJAE
KCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGRITCTSRNRCNDQDTRTSYRI
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/product="hypothetical protein"
/protein_id="CAH18136.1"
/protein_id="CAH18136.1"
/db_xref="q1:51476292"
/translation="MAGGPRRLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVP
/translation="MAGGPRRLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVP
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/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi,
DH10B; sites SfiIA + SfiIB"
YAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNSISVKWLPSSSPVTGYRVTT
TPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVVSVYAQNPSGESQPLVQTAVTTIPA
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_xref="taxon:9606"
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RESULT 13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                          source
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                                                                                                                                                                                                                                       Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                         This clone (DKFZD68601166) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp68601166
Further information about the clone and the sequencing project is
                                                                              available
                                                                                                                                                                                                                                                                                                                                                          Submitted (22-FEB-2005) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Osanger,A., Fobo,G., Han,M. and Wiemann,S. The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens mRNA; cDNA DKFZp68601166 (from BX640875
                                                                                                                                                                                                                                 German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 8411)
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ASTAIDAPSNILRFLATTPNSLLVSWQPFRARITGYIIKYEKSGSPRBYVPRERRGVT
EATTITGLEPGTTEYTIYLALKNNQKSEPLIGRKKTDELPQLVTLPHPNILGPEILDVP
STVQKTPFVTHFOYDTGNGIQLDGTTSGQQDFVGQQMIFEEHGFRRTTPFTTATFIRHR
RRYPFPNVGQEALSQTTISMAPFQDTSEYIISCHPVGTDEEHLGFRVPGTSTSATLTG
LTRGATYNIIVEALKDQQRKVREEVVTVGNSVNEGLNQPTDBSCFDPYTVSHYAVGD
EMERMSESGFKLLQCLLGFGSGHFRCDSSRWCHBUNGYKYGEKWDRQCEGQMNSCT
CLGNGKGEFKCDPHEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCRR
                                                 at http://mips.gsf.de/projects/cdna/
Location/Qualifiers
organism="Homo sapiens"/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (human)
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Pred. No. 2.1e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8411 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTC 23-FEB-2005
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POCUS

ORIGIN

Query Match Best Local Similarity Matches 330; Conserv

Conservative

15.7%; Score 330; DB 4; 1 100.0%; Pred. No. 2.1e-83; tive 0; Mismatches 0;

Length 8411; Indels

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GGGRITGTSRINGUMENT COLLEGE AND THE ACTION OF THE ACTION OF
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GGSEYTVSVVALHDIMESQPLIGTQSTAIPAPTDKETQVTFYSLSAQMTP BNVQLTG
YRVRVTPKEKTGPMKEILLADDSSVUVSGLTVAIKVETVSVYALKDTLTSR BAGGVUT
TLENVS PERRARVTDATETTITISMRTKTETITGEQVDAVPANGQTPIQRTIKEDVRS
YTITGLQPGTDYKIYLYTLNINARSSPVIDASTAIDAPSNIRFATTPNSLLVSWQP
PRARITGYIIKYEKPGS PEREVVPRPREPGVTEATITGLEPGTEYTIYURLAKONQKSE
PLIGRKKTDELPQLVTLAPHNLHGPEILDVBSTVQKTPFVTHFGYDTGMGIQLEGTSG
QOPSUGQMIFEEHGFRRTTPTTTATPITAFPIRREPYPNUGEEIQIGHIFREDVDYHLY
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/db_xref="UniProt/TrEMBL:Q0MZU5"
/db_xref="UniProt/TrEMBL:Q0MZU5"
/translation="MLRGPGPGILLLAVLCGTAVPSTGASKSKRQAQQMVQPQSPVA
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GNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRPHET
                                                                                                                                                    PHGPGLNPNASTGQEALSQTTI SWAPFQDTSEYI I SCHPVGTDEEPLQFRVPGTSTSA
TLTGLTRGATYNI I VEALKDQQRHKVREEVVTVGNSVNEGLNQPTDDSCFDPYTVSHY
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/clone_Tib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
/dev_stage="adult"
NCRRPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNYP1BCFMPLDVQADREDSRB'
                                                          MSCTCLGNGKGEFKCDPHEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCD
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/db xref="InterPro:IPR000562"
/db xref="InterPro:IPR002086"
/db xref="InterPro:IPR003961"
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/protein_id="CAE45932...
/db_xref="GI:34365170"
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/db_xref="RZPD:DKFZp68601166Q"
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ACCESSION
VERSION
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AI095589/c
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465 bp mRNA linear EST 05-OCT-19
gb24a08.x1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone
IMAGE:1697174 3' similar to gb:X02761_cds1 FIBRONECTIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                             Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 446.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.

1 (bases 1 to 465)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMAN);, mRNA sequence.
AI095589
AI095589.1 GI:3434565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                              /clone lib="Soares_pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: pT773-Pac; Site 1: Not i
Site 2: Ecc RI; lst strand cDNA was primed with a Not
oligo(dT) primer [5'
                                                                                                                                                                                                                                                 /clone="IMAGE:1697174"
/sex="female"
                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DH10B"
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.

1 (bases 1 to 734)

1 (bases 1 to 734)

Ota, T., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sugiyama, T., Ota, T., Nakamura, Y., Sugano, S., Masuho, Y. and Isogai, T. Nishikawa, T., Nakamura, Y., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sugiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y., Isogai, T.)

Unpublished (2000)

Contact: Takao Isogai
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AU140802
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Helix Research Institute
Kisarazu, Chiba
                                                                                                                                                                                           Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                             1532-3 Yana, Kisarazu, Tel: 81-438-52-3975 Fax: 81-438-52-3986
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EST.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE4000266"
/tissue_type="placenta"
/clone_lib="PLACE4"
/note="Vector: pME18SFL3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLACE4 Homo sapiens
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                  pME18SFL3"
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Query Match Best Local Sim Matches 329;

h 15.7%; Similarity 99.7%;

Conservative

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Score 329; DB 1; Pred. No. 1.9e-83; 0; Mismatches 1

Length 734; Indels

0

Gaps

B 8	B 8	8 8	B 8	B 8
2004 A   549 A	1944 A   489 A	1884 G       429 G	1824 T 369 T	1764 C 309 C
CAGGCAACG          CAGGCAACG	GAATTGGAGI          GAATTGGAGI	GACGCATCA(	GGGAGAAGC         GGGAGAAGC	CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACG
GCCGAGGAGG           	ACACCTGGAO ACACCTGGAO	CTTGCACTTO	CTACCAAG           CTACCAAG	AGAAGTGTT                   AGAAGTGTTT
AGTGGAAGTO           AGTGGAAGTO	GCAAGAAGGI           GCAAGAAGGI	CTAGAAATA(           CTAGAAATA(	GCTGGATGA:	TTGATCATGO
TGAGAGGCI           TGAGAGGCI	ATAATCGAGO	ATGCAACG           ATGCAACG	NGGTAGATTK           GGTAGATTK	TGCTGGGA(
ACACCTCTGT	HANACCTGCT	ATCAGGACAO	TACTTGCCT	TTCCTATG
rgcagacca          rgcagacca	CCAGTGCA:	CAAGGACATO	rgggagaag          rgggagaag	regtcegagi           regtcegagi
063	003 48	943 88	883 28	1823 368
	N	1944 AGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTGCAGTGCATCTGC	1884 GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACAAAGAACAAGACCATCTTGCACTTCTAGAAATAGATGCAACGATCAGGACAAAGAACAAAGAACATCCTAT	1824 TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCCTACCAAGGCTGGATGATGATTGTACTTGCTTG

Search completed: February 1, 2006, 12:22:51 Job time: 8612.84 secs

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Result
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                       Score
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Match
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12632.698 Million cell updates/sec
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Aar12885 Factor Xa
Ad192189 Streptoki
Aar10194 Streptoki
Aar63120 Streptoki
Aay24794 Streptoco
Aaw94664 Streptoco
Aaw91556 Native st
Aay90282 S. equisi
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## ALIGNMENTS

44444

RESULT 1 AAY24797 Streptococcus; streptokinase; fibrin-dependent plasminogen activator; SKr; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis. N-PSDB; AAX80497 WPI; 1999-395183/33 Synthetic. Streptococcus Streptokinase and maltose binding protein fusion protein. Reed GL; 15-DEC-1997; 15-DEC-1998; 24-JUN-1999. 26-AUG-1999 AAY24797; AAY24797 standard; protein; 795 AA. WO9931247-A1 (HARD ) HARVARD COLLEGE (first entry) dysgalactiae subsp. equisimilis. 98WO-US026694 97US-0069497P

N-terminally

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streptokinase

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated bacterial protein that CC induces fibrin-dependent plasminogen activation in a pharmaceutical CC composition for dissolving blood clots. Also described are: (1) a CC composition comprising an isolated modified streptokinase recomposition comprising an isolated modified streptokinase, the CC modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising CC administering to the subject a fibrin-dependent streptokinase protesing an expression vector comprising (1); and (4) a host cell transformed with CC the expression vector of (3). The pharmaceutical composition comprising a modified bacterial streptokinase; (3) an CC expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving CC blood clots in patients with a thrombosic condition, e.g. myocardial CC infarction, venous thrombosis, plumonary embolism, cerebral thrombosis, CC graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of CC plasminogen is at least 10-fold, preferably 100-fold greater in the CC presence of fibrin than in the absence of fibrin. The modified constrate site for proteolytic cleavage. This reduces the rate of CC degradation of the streptokinase at least two-fold. The present sequence constraint in an example of the present mention.
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                                                  GCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGACAAAGATGGT
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17-SEP-1991
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                                                                                                                                                                                    Xa-cleavable hirudin-IEGR-streptokinase
                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                     IleIleThrValTyrMetGlyLysArgProGluGlyGluAsnAlaSerTyrHisLeuAla
                                                                                                                                                                                                                                                                                                                   GGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGACACCCAACCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrValAspValAsp
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                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                     thrombolysis
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                             70. .483
/label= streptokinase
                                                    'note= "factor Xa cleavage
                                                                                   /label= hirudin HV-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The protein is a recombinant product of a gene fusion construct. The sequence of the synthetic hirudin HV-1 genes was designed based on the published amino acid sequence (Dodt J., et al FEBS Letters 165 180 (1984)). The sequence of streptokinase was obtd. from RCR amplified chromosomal DNA from S. equisimilis ATCC 10009 or ATCC 9642. The primers used for the PCR were based on the pub- lished DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]). The two sequences were used to construct an expression vector in which the hirudin gene is linked to the streptokinase gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also ARR12887-R12889, ARR12891-R12894 and ARR12522. (Updated on 25-MAR-
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N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein cleavage by blood clotting enzyme - for prodn. fractions having greater antithrombotic activity for therapy (
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AACAACAGCCAATTGGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATT
                                                                                                 CACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTT-----
                                                                                                                                            GGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAAGTGTGAGAGG
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                                TyrLeuGlnIleGluGlyArgIleAlaGlyProGluTrpLeuLeuAspArgProSerVal
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90WO-GB001911.
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GluGlyGluAsnAlaSerTyrHisLeuAla
           GAAGGAGAGAATGCTAGCTACCATTTAGCT
                                         TTAACAGCTAGCGAACGTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for harvesting a (poly) peptide produced by a recombinant host cell. The novel method involves selecting a cell comprising a first nucleic acid encoding a leader peptide and a second nucleic acid fragment encoding the desired (poly) peptide. The first and second fragments are within the same open reading frame of the first nucleic acid and the leader peptide is functionally equivalent to an N-terminal leader peptide found with the pre-peptide of a lantibiotic. The host cells and nucleic acids are useful for producing, harvesting and post-translational modification of polypeptides. The polypeptides may be used in the production of pharmaccuticals, e.g. as antigen for vaccine or immunogenic composition. This sequence represents a polypeptide relating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harvesting a desired polypeptide produced by a recombinant host cell, for producing pharmaceuticals, comprises selecting a recombinant nucleic acid comprising nucleic acid fragments encoding a leader peptide and the
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27-NOV-1989;
11-APR-1990;
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                                                                                                                                                                                                                                                                                                                        Synthetic gene encoding streptokinase used as a
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N-PSDB; AAQ10230.
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Streptokinase; SK; Streptococcus myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid comprising a sequence encoding amino acids 14-414 of streptchinase, which binds to plasminogen and does not have a sequence comprising amino acids 60-414 is new. The polypeptide pref. comprises amino acids 244-352, 1-352, 120-352 or 244-414. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a polypeptide which binds to plasminogen and corresponds region of streptokinase - useful to detect plasminogen in a sample and treat myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated bacterial protein that CC induces fibrin-dependent plasminogen activation in a pharmaceutical CC composition for dissolving blood clots. Also described are: (1) a CC composition tomprising an isolated modified streptokinase, the CC modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising CC administering to the subject a fibrin-dependent streptokinase protein; a CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an CC expression vector of (3). The pharmaceutical composition comprising a compression vector of (3). The pharmaceutical composition comprising a blood clots in patients with a thrombotic condition, e.g. myocardial cC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, CC graft thrombosis and arterial thrombosis. The modified streptokinase can CC also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the cc presence of fibrin than in the absence of fibrin. The modified constrate site for proteolytic cleavage. This reduces the rate of CC degradation of the streptokinase at least two-fold. The present sequence CC represents native by field) protection of strandardise by field)
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                                                                                                                                                                                                                                                                         The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence represents native SK. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPlg) to plasmin (HPlm), which is a serine protease able to catalyse the hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen. (Updated on 17-OCT-2003 to standardise OS field)
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      IleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAsp

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                                                                                                                                                                                                                                                    Alignment
                                                                                                                                                                                                                                                                                      The present sequence represents a native streptokinase. The specification describes a polypeptide which binds to a streptokinase specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase-specific antibody and reduces therapy, and to prevent or treat glomerulonephritis and rheumatic fever. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                      Sequence 414
                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides which thrombolytic therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aurigenic peptide; streptokinase; streptokinase-specific antibody; thrombolytic activity; thrombolytic therapy; glomerulonephritis; rheumatic fever.
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Streptokinase; SK; hybrid plasminogen activator; fibrin plasminogen; human; fibronectin; thrombolytic therapy;
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                                                                                                                                                                                                                                                                                                                                                                                             CC plasminogen activator (PA) comprises a polypeptide fusion between conditions (SK), which are capable of plasminogen (PG) activation, and C fibrin binding regions of human fibronectin, which are from fibrin cC binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the C ability to bind with fibrin independently and also characteristically C retains a PG activation ability which becomes evident only after a C pronounced duration, or lag, after exposure of the PA to a suitable C animal or human PG. The hybrid streptokinase-fibrin binding domain C polypeptides are useful in thrombolytic therapy for various kinds of C cardiovascular disorders. The hybrids have enhanced fibrin selectivity as C well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of C plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins C can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating C blood plasminogen to plasmin, thus aidling in the localisation of the C plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation encountered during clinical use of streptokinase. (Updated on 12-SEP-2003 to standardise OS field)
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Yadav M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin.
                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                        Sequence 414
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                                                                                                                              CATTTAGCT 1736
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                                                                                                                                                                                                                                                                                                        TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTT
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                                                                                                                                                                                                                                                                       The conjugate comprises an FB-FB dimer linked to streptokinase The FB fragment has selective affinity for fibrin, low affinity for fibrinogen, and minimal immunogenicity, imparting thrombus- targetting capability. See also AAR11821 and AAR11828
                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 5; 18pp; English
                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-140198/19.
N-PSDB; AAQ11651.
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CTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACTTTGAG
                          injectable fibrinolytic agent - with affinity for intravascular by linking agent to fibrin binding domain.
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fusion protein.
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 Streptococcus equisimilis H46A; streptokinase; mutant;
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                                                                                                                                               GACACCAACCGTATCATAACCGTTTATATGGGCAAGGGACCCGAAGGAGAGAATGCTAGC 1724
                                                                                                                                                                        CTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGAT 166-
                                                                                                                                                                                                          AsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsn
                                                                                                                                                                                                                   AACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAAT
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                                                                                                                                                                                                                                                                                                                                                 GAGTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGT 1364
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                                                                                                                                                                                                                                                                                              GGGGAAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATAC 1484
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                  mutant
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                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the ProSB-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence is mutant SK K59E. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPlm), which is a serine protease able to catalyse the plasmin (HPlm), which is a serine protease able to catalyse the hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 414
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N-PSDB; AAX16633.
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                                                                                                                              AGCGTTGCTGGTGACTGTTGAGGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAATC
                                                                                                                                                                                               ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT
                        AAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTGAGGTC
                                                                                                                                                                                 IleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal
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                                                                                                                                             HisLeuAla
                                                                                                                                                                     CATTIAGCT 1736
                                                                                                                                                                                               ThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGlyGluAsnAlaSerTyr
                                                                                                                                                                                                              AspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAsp
                                                                                                                                                                                                                                                               GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC
                                                                                                                                                                                                                                                                                                     LeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeu
                                                                                                                                                                                                                                                                                                               TTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTC 1607
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                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                           The protein is a recombinant product of a gene fusion construct. The sequence of the synthetic hirudin HV-1 genes was designed based on the published amino acid sequence (Dodt J., et al FEBS Letters 165 180 (1984)). The sequence of streptokinase was obtd. from PCR amplified chromosomal DNA from S. equisimilis ATCC 10009 or ATCC 9642. The primers used for the PCR were based on the pub- lished DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]). The two sequences were used to construct an expression vector in which the streptokinase gene is linked to the hirudin gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also AAR12887-R12889, AAR12891-R12894 and AAR12885. (Updated on 25-MAR-
                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                          Sequence 483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 96; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion protein cleavage by blood clotting enzyme - for prodn. fractions having greater antithrombotic activity for therapy (
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     GATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAAATCA
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/note= "factor Xa cleavage
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/label= streptokinase
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CATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAGACCCTACCAAGGCTGG
                                                                                          CATTTAGCTGGTGGTCGCCAGGCGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGAT
                                                                                                                                                AspālaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspāsnHisāspāsp
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                                         HisLeuAla-----TyrAspLysAspArgTyrThrGluGluArgGluValTyrSer 398
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This sequence represents a fusion protein between maltose-binding protein and the plasminogen-binding fragment of streptokinase. This fusion protein was used in the design of modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, optionally as a bolus rather than by continuous infusion. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                     Example 1;
                                                                                                                                                                                                                     Modified
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17-SEP-1991
The streptokinase sequence was obtd. from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C) ATCC 10009 or ATCC 9642 (the primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]). The gene was fused to DNA encoding the yeast alpha factor pre-pro-secretion sequence in an expression vector, pSMD1/152, fc prodn. of recombinant strepto- kinase in S. cerevisiae strain BJ2168. Se
                                                                                                          fractions having greater prophylaxis.
                                                                                        Disclosure; Page
                                                                                                                    Fusion protein cleavage by blood clotting enzyme - for prodn. fractions having greater antithrombotic activity for therapy a
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                                                                                                                                                                                                                                                                                                                                       /label= pre-pro ; /note= "S. cerev 86. .499
                                                                                                                                                                                                                                                                                                                                                                                                                               blood clotting
thrombolysis;
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ATAAACAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAAAAAAGGGGAAAAGCCCG
                               ValGlnPheThrProLeuAsnProAspAspAspPheArgProGlyLeuLysAspThrLys
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                                                                                      This sequence represents the wild type plasminogen-binding fragment of streptokinase. This fragment was used in the design of a modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, opt. as a bolus rather than by continuous infusion. (Updated on 17-0CT-2003 to standardise OS field)
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01-OCT-1997
                                                                Sequence 813
                                                                                                                                                                                                                                             Modified
                                                                                                                                                                                                                                                                      WPI; 1997-065469/06
                                                                                                                                                                                                                                                                                                                                                09-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
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                                                                                                                                                                                                                            lified forms of streptokinase resistant to enzymatic cleavage - useful thrombolytic agents in treating thrombosis and in medical equipment.
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                                                             GATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAAC 1547
                                                                                                   GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal
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Search completed: January 28, 2006, 02:09:01 Job time : 167.802 secs	380 HisLeuala 382	1728 CATTTAGCT 1736	360 ThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGlyGluAsnAlaSerTyr 379	1668 ACCAACCGTATCATAACCGTTTATATGGGCAAGCGACCCGAAGGAAG	340 AspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAsp 359	1608 GATGCTTTTGGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGAC 1667

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Minimum DB
Maximum DB
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-Q=/cgn2 1/USPTO spool p/US09940235/runat 27012006 144219 27602/app_query.fasta_1.7708
-Q=/cgn2 1/USPTO spool p/US09940235/runat 27012006 144219 27602/app_query.fasta_1.7708
-DB=Issued_Patents AA -OFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN-0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09940235 GCGN 1 1159 @runat 27012006 144219 27602 -NCPU-6 -ICPU-3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Perfect score:
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Maximum Match 10
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length: 2000000000
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/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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         Patent No. 5240845
Sequence 52, Appl
Sequence 47, Appl
Sequence 1, Appli
Sequence 28, Appli
Sequence 3, Appli
Sequence 26, Appli
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Sequence 43, Appl
Sequence 264, Appl
Sequence 6, Appli
Patent No. 5240845
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Sequence
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US-09-211-542A-2
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## ALIGNMENTS

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Sequence 2, Application US/09211542A Patent No. 6210667
GENERAL INFORMATION:
                    TELEPHONE: (617)443-9292
TELEPAX: (617)443-0004
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
                                                                                REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES:
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                                                                                                                           NAME: Attorney, Strimpel, Harriet REGISTRATION NUMBER: 37,008
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; LENGTH: 795 amino ac:
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; Sequence 43, Application US/07854596B
; Patent No. 5434073
; GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
; APPLICANT: Hunter, Michael G
; APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nu
NUMBER OF SEQUENCES: 73
                                                                                                                                        ; LENGTH: 483 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-854-596B-43
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION UNDERE: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPAN: 312-715-1000
TELEPAN: 312-715-1000
TELEPAN: 312-715-1234
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acid
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ADDRESSEE: Dr. John J. McDonnell
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Patent No. 6861236
GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification
FILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: ED-2077060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: PatentIn version 3.1
SEQ ID NO 264
LENGTH: 413
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; Sequence 6, Application US/09211542A
; Patent No. 6210667
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Strimpel, Harri
REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/1
TELECOMPUNICATION INFORMATION:
TELEPHONE: (617)443-9292
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, Guy L.
TITLE OF INVENTION: BACTERIAL FIBI
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMBERG & SUNSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
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STATE: Massachusetts
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RESULT 5
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; APPLICANT: FUJII, SETSURO;T.;MAJIMA, EIJI;OGINO, KOICHI;ONO,;TSUTOMU
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                                                          TITLE OF INVENTION: MUTATED STREPTOKINASE NUMBER OF SEQUENCES: 65
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/549,049
FILING DATE: 06-JUL-1990
                                            LENGTH:
                                                      NO:1:
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; Sequence 52, Application
; Patent No. 5976841
; Patent No. 17770177771
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                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATB: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATB: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELEPHONE: (202) 628-8844
TELEPHONE: (202) 628-8844
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INFORMATION FOR SEQ ID NO: !
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ADDRESSEE: Evenson, Mc
STREET: 1200 G Street,
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEPFENS, Gerd Josephan
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
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LENGTH: 440 amino acids
                                                                                                                                 No.:
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Pred. No.:
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US-07-854-596B-47
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                                                                                                                                                                                                                                                                                                                                                                                                       NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1234
TELEPAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 47:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                         Local Similarity:
y Match:
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
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78.94%
53.09%
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                                           ValValTyrThrAspCysThrGluSerGlyGlnAsnLeuCysLeuCysGluGlySerAsn 438
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Best Local Similarity:
Query Match:
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US-08-488-940-1
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                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION UNMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPB: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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COMPUTER READABLE FORM:
MEDIUM TYPB: Floppy
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/488,940
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RESULT 9
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                                        TATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCACCATCAAATACGTTGATGTCGAT 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                GlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAspThrAsnArg
                                                                                                             GGTATTATGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGACACCAACCGT 1678
                                                                                                                                                    ArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPhe
                                                                                                                                                                 AGAGATTTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTT
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Sequence 28, Application US/07854596B
Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucl
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Su:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SESTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDONNell, John J
REGISTRATION UNUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION 1076
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1000
TELEPAX: 312-715-1334
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COUNTRY:
ZIP: 606
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CITY: Chicago
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                                                                 GCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGACTTACTAAAGGCTATT
                                                                                        SerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSerLysProPhe
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US-08-488-940-3
; Sequence 3, Application
; Patent No. 5854049
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                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pish & Richardson
STREET: 225 Franklin Street
  COMPUTER READABLE FORM:
                                ADDRESSEE:
STREET: 22:
CITY: Bosto
STATE: MA
          COUNTRY: USA
ZIP: 02110-2804
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GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
TO THE TOTAL PROPERTY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/488,940 FILING DATE: 09-JUN-1995 CLASSIFICATION: 514
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                                                   GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 1127
                                                                                                              GTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG 1067
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                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                      ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                ATTORNEY/AGENT INFORMATION:
NAME: MCDOMNE11, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                         STREET: Ten So
CITY: Chicago
STATE: IL
                                                                                              APPLICATION NUMBER: US/07/854,596B FILING DATE: 03-JUN-1992
                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dr. John J. McDonnell
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DB:
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TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
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                                                              TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
                                                                                               AlaGlnAlaGlnSerIleLeuAsnLysThrHisProGlyTyrThrIleTyrGluArgAsp
                                                                                                            GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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                                               SerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu
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Matches:
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; Sequence 19, Application US/07854596B
; Patent No. 5434073
; GENERAL INPORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
ITITLE OF INVENTION: Proteins and nu
NUMBER OF SEQUENCES: 73
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                 Pred. No.:
                           Alignment Scores:
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                                                        US-07-854-596B-19
                                                                                 TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/854,596B
                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
CITY: C
                                                                                                                                                                                                                                                                    FILING DATE: 03
CLASSIFICATION:
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DB:
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                                                                       GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrVal
                                                                                                              AsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLysGly
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Percent Similarity:
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Query Match:
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US-07-854-596B-15
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acide
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTINE PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 292,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
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APPLICANT: Dawson,
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and
NUMBER OF SEQUENCES: 73
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                                                                                                                                                                                                                                                                                                                                          LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ZIP: 60606
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TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
TELEFAX: 312-715-1234
TELEFAX: 910-221-5317
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Patent No. 5434073
GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73
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COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596E
FILING DATE: 03-UN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
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ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive,
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ATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGAC

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RESULT 15
US-08-488-940-18
                                                                                        Sequence 18, Application US/08488940
PATENT NO. 5854049
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESIS
NUMBER OF SEQUENCES: 20
                                                                           CORRESPONDENCE ADDRESS:
STREET: 225 F.
CITY: Boston
STATE: MA
COUNTRY: USA
                                                              ADDRESSEE:
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TELEPAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/488,940 FILING DATE: 09-JUN-1995 CLASSIFICATION: 514
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             AGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTGGAATATACT 1076
                                                                          TCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTGCTAAGCGGACATGTGCGCGGTT 1016
                                                                                                                                        GCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTGCTGACAAAGATGGT 956
                                                                                                                                                                                                       GlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPheGluValIleAspPhe
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eAspLeuThrSerArg
                     AGATGCAACGATCAGG 1926
                                         SerValAlaGlyThrValGluGlyThrAsnGln-AspIleSerLeuLysPhePheGluIl
                                                                                   TyrThrGlyThrProIleProAspAsnProAsnAspLysAsnAsnSerGlnLeuValVal
                                                                                                          GGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCCTACCAAGGCTGGATGATGGTA 1856
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Result
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-DB=Published Applications AA Main -QFMT=fastan -SUFFIX=rapbm -MINMATCH=0.1
-LOOPEXT=0 -UNITS=blis -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORB=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US09940235 eCGN 1 1 805 @runat 27012006 144219 27635
-NCPU=6 -ICPU=3 -NO MARP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOD=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB
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Maximum Match 10
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-MODEL=frame+_n2p.model
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length: 2000000000
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Ygapop 10.0 , Ygapext
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3726
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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first 45 summaries
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   US-10-360-101-264

US-09-940-235-2

US-10-300-215-252

US-10-988-943-1

US-10-300-215-253

US-09-919-703-12

US-10-474-792-658

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Sequence 264, App
Sequence 2, Appli
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Sequence 13, App
Sequence 12, Appli
Sequence 12, Appl
Sequence 658, App
Sequence 658, App
Sequence 215, App
Sequence 216, Appl
Sequence 1, Appli
Sequence 206, App
Sequence 4, Appli
Sequence 4, Appli
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(D	equence 107	equence 32,	e 360	equence 28,	equence 1	equence 436,	e 147,	equence	e 1067,	e 104,	е 366,	e 357,	e 94	æ	e 10	8	Sequence 1075, Ap	е 36	4		35	1072	359	Sequence 677, App	677		98	98		equence 64,	equence 2,	•

## ALIGNMENTS

RESULT 1 US-10-360-101-264

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; Sequence 264, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
TITLE OF INVENTION. Export and modification of (poly) peptide in the lantibiotic way
FILE REFERENCE: 2183-5673
CURRENT PHILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02077060.8
PRIOR FILING DATE: 2003-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 264
LENGTH: 413
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER IMFORMATION: sequence of streptokinase
US-10-360-101-264
Alignment Scores:
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Best Local Similarity: 100.00%
Best Local Similarity: 100.00%
DB:
US-09-940-235-12 (1-2096) x US-10-360-101-264 (1-413)
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APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Ka
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RESULT 3
US-10-300-215-252
US-10-300-215-252
; Sequence 252, Application No. US200:
; Publication No. US200:
; GENERAL INFORMATION:
APPLICANT: ADAIR, Fiona Suzame
APPLICANT: HAMILTON, Anita Anne
APPLICANT: CARTER, Graham
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
TITLE OF INVENTION: NON-INMUNOGENIC PROTEINS
FILE REFERENCE: MER-104-Con.1
CURRENT APPLICATION NUMBER: US(10/300,215
CURRENT FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US 09/438,136
PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
PRIOR FILING DATE: 1998-05-21
PRIOR PRIOR APPLICATION NUMBER: GB 9710480.6
PRIOR FILING DATE: 1997-05-21
PRIOR APPLICATION NUMBER: GB 9716197.0
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; PRIOR APPLICATION NUMBER: GB 9725270.4
; PRIOR APPLICATION NUMBER: GB 9807751.4
; PRIOR APPLICATION NUMBER: GB 9807751.4
; PRIOR FILING DATE: 1998-04-14
; PRIOR PRILING DATE: 1998-04-14
; PRIOR PILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
organism: Streptococcus equisimilis
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Conservative:
Mismatches:
Indels:
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Sequence 1, Application US/10988943

Publication No. US20050176085A1

GENERAL INFORMATION:
APPLICANT: Center for Genetic Engineering and Biotechnology
TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF ITILE OF INVENTION: COMPLEX MIXTURES.
FILE REFERENCE: Proteomics CU2003-269
CURRENT APPLICATION NUMBER: US/10/988,943
CURRENT APPLICATION NUMBER: US/10/988,943
CURRENT FILING DATE: 2004-11-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 415
TYPE: PRT
ORGANISM: Streptococcus equisimilis
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Best Local Similarity:
Query Match:
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; Publication No. US20030153043A1
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Query Match:
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PRIOR APPLICATION NUMBER: WO PCT/GB98/0147
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: GB 9710480.6
PRIOR PILING DATE: 1997-05-21
PRIOR APPLICATION NUMBER: GB 9716197.0
PRIOR APPLICATION NUMBER: GB 9725270.4
PRIOR FILING DATE: 1997-07-31
PRIOR PILING DATE: 1997-11-28
PRIOR PILING DATE: 1997-11-28
PRIOR FILING DATE: 1997-12-27
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 254
SOFTWARE: PASKSEQ for Windows Version 4.0
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LENGTH: 414
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TITLE OF INVENTION: MCHIND FOR THE PRODUCTION
TITLE OF INVENTION: WON-IMMUNOGENIC PROTEINS
FILE REFERENCE: MER-104-Con.1
CURRENT FAPPLICATION NUMBER: US/10/300, 215
CURRENT FALLING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US 09/438,136
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ORGANISM: Artificial
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IOR FILING DATE: 1999-11-10
IOR APPLICATION NUMBER: WO PCT/GB98/01473
IOR FILING DATE: 1998-05-21
IOR APPLICATION NUMBER: GB 9710480.6
IOR APPLICATION NUMBER: GB 9716197.0
IOR APPLICATION NUMBER: GB 9716197.0
IOR FILING DATE: 1997-07-31
IOR APPLICATION NUMBER: GB 9725270.4
IOR APPLICATION NUMBER: GB 9807751.4
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      IleaspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAsp

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                                                            APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Peptides and Their Use t
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/003004
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR PILING DATE: 1995-12-06
PRIOR PILING DATE: 1995-12-06
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NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 413
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                    GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 1127
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Mismatches:
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Publication No. US20040236072A1

GENERAL INFORMATION:
APPLICANT: Olmsted, Stephen
APPLICANT: Nickbarg, Elliot
APPLICANT: Nickbarg, Elliot
APPLICANT: Winter, Lourie
TITLE OF INVENTION: SURFACE PROTEINS OF STRE
FILE REFERENCE: AM 100399

CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14

NUMBER OF 520 ID NOS: 674

SOFTWARE: PatentIn version 3.0

SEC ID NO 658
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; TYPE: PRT
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RESULT 6
US-10-35
Sequence 235, Application US/10360101
Publication No. US20040009550A1
GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02077060.8
                                         APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification
FILE REFERENCE: 2183-5673
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; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 235
; LENGTH: 2355
; TYPE: PRT
; ORGANISM: Artificial Sequence
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                                                                                                                      hrSerValGlnThrThrSerSerGlySerGlyProPheThrAspValArgAlaAlaValT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACGGTTTCCCTCTAGAA----ATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCAACGCTGCCCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGCCAGCCTAGCCGGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGGCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspCysThrCysIleGlyAlaGlyArgGlyArgIleSerCysThrIleAlaAsnArgCys 110
                                                                   yrGlnProGlnProHisProGlnProProProTyrGlyHisCysValThrAspSerGlyV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oHisGluThr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGlyLysGlyGlu-TrpThr----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TCGCTCGCGTATCGGTGATTCATTCTGCTAACCAGTAAGGCAACC
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                                         GGACCTGAGTGGCTAGACCGTCCATCTGTCAACAACAGCCAAT 639
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Matches:
Conservative:
Mismatches:
Indels:
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1743	CCGTTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGCTA	1684
465	etTyrargIleGlyAspGlnTrpAspLysGlnHisAspMetGlyHisMetMetArgC	446
1683	TGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGACACCCAACCGTATCATAA	1624
446	III:::  GlyValm	444
1623	TATACGATCCTCGTGATAAGGCTAAACTACTCCTACAACAATCTCGATGCTTTTGGTATTA	1564
443	:::      :::::      :::    roMetAlaAlaHisGluGluIleCysThrThrAsnGlu	431
1563	AATTGCTAAAAAGTGAGCAGCTCTTAAÇAGCTAGCGAACGTAACTTAGACTTCAGAGATT	1504
431	Phe	411
1503	ACTTGAAACTGTTCACCATCAAATACGTTGATGTCGATACCAACG	1459
411	erGluGlyArgArgAspA	405
1458	CTGAGAAATATTACGTCCTTAAAAAAAGGGGAAAAGCCCGTATGATCCCTTTTGATCGCAGTC	1399
405		399
1398	CTTATAGGATCAATAAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCT	1339
398	PheProPheLeuTvrAsnAsnHis	391
1338	TCCGTACGATTTTACCAATGGATCAAGAGTTTACTTACCGTGTTAAAAATCGGGAACAAG	1279
390		382
1278	ACCCAGGCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTT	1219
381		376
1218	GTGÁCACCATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAAACC	1159
375		375
1158	CTGATGACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAAACACTAGCTATCG	1099
375	-GlnAspGlnLysTyrSerPheCysThrAspHisThrVal	363
1098	TACAAAACCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAAACC	1039
362		359
1038	CTGTCCAAGAATTTTTTGCTAAGCGGACATGTGCGCGTTAGACCATATAAAGAAAAACCAA	979
359	hrPheTyrSerCysThrThrGluGlyArgGlnAspGlyHisLeuTrpCysSerThrThrS	339
978	TCTACTTTTGCT	934
339	lyGluProCysValLeuProPheThrTyrAsnGlyArgT	326
933	TTGAGGTCATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGG	880
326		311
879	ACTTACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACT	820
310		310
819	CAAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTG	760
310	:::    AsnGlyValSer-	307
759	TTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGAGAG	700
306	etLeuCysThrCysLeuGly	300
699	TGGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTT	640

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GENERAL INFORMATION:

APPLICANT: HB-STUMEP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOEN
APPLICANT: KRAETZSCHMAR, JOEN
APPLICANT: KRITSCHMAR, JOEN
APPLICANT: WINTERHAGER, ELKE
APPLICANT: WINTERHAGER, ELKE
APPLICANT: SCOTTI, SIMONE
ITILE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARB: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-961-403-1
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Pred. No.:
                                                                                                                                                                                                                          US-09-940-235-12 (1-2096) x US-09-961-403-1 (1-2386)
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-961-403-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09961403
Publication No. US20030077589A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2386
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1978 GAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGA 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1918 ACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATC 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1798 GGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCCTACCAAGGCTGGATGATGGTAG 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1744 GCCAGGCGCAACAGATTGTA-----CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTG 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 -- GlyValArgTyrGlnCysTyrCysTyrGlyArgGlyIleGlyGluTrpHisCysGln- 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531 lnAspSerGluThrGlyThrPheTyrGlnIleGlyAspSerTrpGluLysTyrValHis- 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 spīleThrTyrAsnValAsnAspThrPheHisLysArgHisGluGluGlyHisMetLeuA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 lyGluTrpThrCysIleAlaTyrSerGlnLeuArgAspGlnCysIle-----ValAspA 491
 157 oHisGluThr --
                                   107 CCGCCAGCCTAGCCGGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGGCCAGGA 166
                                                                    142 HisGluGlyGlyGlnSerTyr-LysIleGlyAspThrTrp-----ArgArgPr 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          570 -----ProLeuGlnThrTyrProSerSerSerGlyPro 580
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465 ysThrCysValGlyAsn-----
                                                                                                                                                                                     5 GACCATTCATGTTGCTCAGGTCGCAGACGTTTTGCAGCAGCAGTCGCTTCACGT---
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                                                                                                           TCGCTCGCGTATCGGTGATTCATTCTGCTAACCAGTAAGGCAACC 106
                                                                                                                                                                                                                                                                                 Conservative: Mismatches: Indels:
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--GlyArgG
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1039 TACAAAACCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAAACC 1098    :::        ::::    394GlnAspGlnLysTyrSerPheCysThrAspHisThrVal	979 CTGTCCAAGAATTTTTGCTAAGCGGACATGTGCGCGTTAGACCATATAAAGAAAAACCAA 1038 	ACAAAGATGGTTCGGTAACCTTGCCGACCCAAC :::       ::: rgGlnAspGlyHisLeuTrpCysSerThrThrS	TTGAGGTCATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGG	820 ACTTACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACTACT 879         ::: 342CysGlnGluThrAlaValThrGlnThrTyrGlyAsnSerAsnG 357		TTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTC	640 TGGTTGTTAGCGTTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTT 699 :::: ::     331 etLeuCysThrCysLeuGly		593 593 294 yrGlnProGlnProHisProGlnProProProTyrGlyHisCysValThrAspSerGlyV 314			AGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAA		344 CCTATGTGGTCGGAGAAACGTGGGA368 	284 TGCAAGCACAACAGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGCGGGACTT 343	227 CAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGAGATATACCATGG 283	167 CCCAACGCTGCCCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCA 226
RESULT 10 US-10-788-792-206 US-10-788-792-206 ; Sequence 206, Application US/10788792 ; Publication No. US20040191819A1 ; GENERAL INFORMATION: ; APPLICANT: Bayer Pharmaceuticals Corporation	Qy 2038 GGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCC 2078 :::	Qy 1978 GAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGA 2037	Qy 1918 ACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATC 1977	Qy 1858 ATTGTACTTGCCTGGGAGAAGGCAGCGACGACCATCACTTGCACTTCTAGAAATAGATGCA 1917	Qy 1798 GGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAG 1857	Qy 1744 GCCAGGCGCAACAGATTGTACCCATAGCTGAAAAGTGTTTTGATCATGCTGCTG 1797   :::	Oy 1684 CCGTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTACCATTTAGCTGGTGGTG 1743 :::	- 19 19 19	Oy 1564 TATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTTGGTATTA 1623	1504 AAT : 462 rom	Qy 1459 ACTTGAAACTGTTCACCATCAAATACGTTGATGTCGATACCAACG 1503	Oy 1399 CTGAGAAATATTACGTCCTTAAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTC 1458	Qy         1339 CTTATAGGATCAATAAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCT 1398	Qy 1279 TCCGTACGATTTTACCAATGGATCAAGAGTTTACCTTACCGTGTTAAAAATCGGGAACAAG 1338	Oy 1219 ACCCAGGCTATACGATTTATGAAACGTGACTCCTCAATCGTCACTCAC	1159 GTGACACCATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAAACC	406

Db 294 yrGlnProGlnProHisProGlnProProProTyrGlyHisCysValThrAspSerGlyV 314	Qy 593 593	Oy 538 CCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCCTTCACCGATGTTCGTATTGCT 593	Qy 478 ACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACA 537	234		Qy 369GAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATC 417		344 CCTATGTGGTCGGAGAAACGTGGGA	OY 284 TGCAAGCACAACAGATTGTACCCATAGCTGACAAGTGTTTTGATCATGCTGGGGGACTT 343	161 -GlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGlyLysGlyGlu-TrpThr	QY 227 CAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTATTAAGAAGGAGATATACCATGG 283	Db 160 160	QY 167 CCCAACGCTGCCCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCA 226	::: 157 OHisGluThr	107 CCGCCAGCCTAGCCGGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGGCCAGGA	Qy 62TCGCTCGCGTATCGGTGATTCTGCTAACCAGTAAGGCAACC 106	Db 122 AspCysThrCysIleGlyAlaGlyArgGlyArgIleSerCysThrIleAlaAsnArgCys 141		US-09-940-235-12 (1-2096) x US-10-788-792-206 (1-2386)	/ Match: 17.148	t Similarity: 36.69% Conservative:	Length:	Alicament Compos.	; ORGANISM: Homo sapiens	70		; PRIOR APPLICATION NUMBER: US 60/450,655 ; PRIOR FILING DATE: 2003-02-28	; FILE REFERENCE: 5152 ; CURRENT APPLICATION NUMBER: US/10/788,792 ; CURRENT FILING DATE: 2004-02-27	; APPLICANT: Bigwood, Douglas; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE	; APPLICANT: Eveleigh, Deepa
Db	Q	D 45	₹ B	& B	. S	рь	Q B	Ş	Db	γQ	F 8	Φb	Qy .	Db	γQ	Db	Q Q	당 &	D Db	Ş	Db	Q	Db	δ	D .	Ş Ş	Db .	\$ 8	Qy	_
475GlyValm 477	TATTA  :::	roMetAlaAlaHisGluGluIleCysThrThrAsnGlu	:::::    snMetLysTrpCysGlyThrThrGlnAsnTyrAspAlaAspGlnLysPheGlyPheCy snMetLysTrpCysGlyThrThrGlnAsnTyrAspAlaAspGlnLysPheGlyPheCy	436 erGluGlyGITTCACCATCAAATACGTTGATGTCGATACCAACG 1503	CTGAGAAATATTACGTCCTTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTC		422 429  1339 CTTATAGGATCAATAAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCT 1398	TCCGTACGATTTTACCAATGGATCAAGAGTTTACTTACCGTGTTAAAAATCGGGAACAAG	413	ACCCAGGCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTT	1159 GTGACACCATCACATCTCAAGAATTACTGCCTCAAGCACAAAGCATTTTAAACAAAAACC 1218		CTGATGACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCG		1039 TACAAAACCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAAACC 1098	erAsnTyrGlu	CTGTCCAAGAATTTTTGCTAAGCGGACATGTGCGCGTTAGACCATATAAAGAAAAACCAA	934 TCTACTTTGCT	lyGluProCysValLeuProPheThrTyrAsnGlyArgT	TTGAGGTCATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGG	342CysGlnGluThrAlaValThrGlnThrTyrGlyGlyAsnSerAsnG 357	820 ACTTACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACT 879	341 341	760 CAAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTG 819	:::     AsnGlyValSer-	TTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTC	etLeuCysThrCysLeuGly	314 alValTyrSerValGlyMetGlnTrpLeuLysThrGlnGlyAsnLysGlnM 331		

Oy  5 GACCATTCATGTTGTTGCTCAGGTCGCAGACGTTTTGCAGCAGCAGTCGCTTCACGT 61     :::   :::	Alignment Scores: 7.49e-49 Length: 2386 Pred. No.: 638.50 Matches: 208 Score: 638.50 Matches: 69 Percent Similarity: 36.69% Conservative: 69 Best Local Similarity: 27.55% Mismatches: 151 Query Match: 17.14% Indels: 328 DB: 5 Gaps: 28  US-09-940-235-12 (1-2096) x US-10-868-577A-59 (1-2386)		Qy 1624 TGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGACACCGAACCGTATCATAA 1683
Qy 979 CTV	3420 3420 357	Qy 107 CO Db 157 oH Qy 167 CC Db 160 Qy 227 CA Db 161 -G Qy 284 TG Qy 344 CC Qy 344 CC Qy 369 Db 234 In Db 254 Sn Db 274 hr Qy 593 Qy 593 Qy 593 Qy 700 TD Db 331 etc Qy 760 CA	1 1 4 2
CTGTCCAAGAATTTTTGCTAAGCGGACATGTGCGGTTAGACCATATAAAGAAAAAACCAA 1038	TATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACGACTACT	CCGCCAACGCTMGCCGAGTCCTCAACGACCACGACCACCACCACCACCCCTGGCCACCCCGTGGCCACCCCGTGGCCACCCCTGGCCACCCCTGGCCACCCAC	:::        :::::

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1744
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                                                                                                                                     GAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGA 2037
                                                                                                                                                                               TGGACTATACCTTAACTGGAAAAGTAGAGGATAATCACGATGACACCAACCGTATCATAA 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIGAAA---CTGTTCACCATCAAATACGTTGATGTCGATACCAAC------G
                                               GGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCC 2078
                                                                                                                                                                                                                                                                                                                                                                    spIleThrTyrAsnValAsnAspThrPheHisLysArgHisGluGlyHisMetLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCAGGCGCAACAGATTGTA-----CCCATAGCTGAGAAGTGTTTTGATCATGCTGCTG 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATC 1977
                                                                                                                                                                                                                                                                            snCysThrCysPheGlyGlnGlyArgGlyArgTrpLysCysAspProValAspGlnCysG 562
                                                                                                                                                                                                                                                                                                                                                                                                                    GGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCCTACCAAGGCTGGATGATGGTAG 1857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTTGGTATTA 1623
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                                                                                          --GlyValArgTyrGlnCysTyrCysTyrGlyArgGlyIleGlyGluTrpHisCysGln- 600
                                                                                                                                                                                                                                                                                                                         ATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCA 1917
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lyGluTrpThrCysIleAlaTyrSerGlnLeuArgAspGlnCysIle-----ValAspA 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 et---TyrArgIleGlyAspGlnTrpAspLysGlnHisAspMetGlyHisMetMetArgC
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    -ProLeuGlnThrTyrProSerSerSerGlyPro 611
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Publication No. US20050129681A1

GENERAL INFORMATION:
APPLICANT: Varner, Judith A.
TITLE OF INVENTION: Methods for Inhibiting Angiogenesis
FILE REFERENCE: UCSD-07325

CURRENT APPLICATION NUMBER: US/10/485,758

CURRENT FILING DATE: 2004-02-03

PRIOR APPLICATION NUMBER: 60/310,645

PRIOR APPLICATION NUMBER: 60/310,645

PRIOR FILING DATE: 2001-08-06

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn version 3.1
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; LENGTH: 2386
; TYPE: PRT
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                                                                                                                                                          234 lnAspThrArgThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyA 254
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                                                                                       ACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACA
                                                                                                                                                                                  AGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAA 477
                                                                                                                                                                                                                                                                                                                                                                                       CCTATGTGGTCGGAGAAACGTGGGA-----
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US-09-940-235-12 (1-2096) x US-10-485-758-9 (1-2386)  Qy	8apiens 7. 63 36 ty: 27	RESULT 13  US-10-485-758-9  ; Sequence 9, Application US/10485758  ; Publication No. US20050129681A1  ; GENERAL INFORMATION:  ; APPLICANT: Varner, Judith A.  ; TITLE OF INVENTION: Methods for Inhibiting Angiogenesis  ; FILE REFERENCE: UCSD-07325  ; CURRENT PAPLICATION NUMBER: US/10/485,758  ; CURRENT PAPLICATION OF CONTROL OF CO	Qy 1858 ATTGTACTTGCCTGGGAGAAGGCAGCGATCACTTGCACTTCTAGAAATAGATGCA 1917 :::	Qy 1564 TATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTTGGTATTA 1623  Db 475GlyValm 477  Qy 1624 TGGACTATACCTTAACTGGAAAAGTAGAAGGATAATCACGATGACCAACCGTATCATAA 1683

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; LENGTH: 2320 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-236-392-2  Alignment Scores: 1.26e-48 Length: 2320 Pred. No.: 636.00 Matches: 205 Score: 636.00 Matches: 71 Percent Similarity: 36.56% Conservative: 71 Best Local Similarity: 27.15% Mismatches: 154	אוס די	FILING DATE: 2002-03-25 APPLICATION NUMBER: US60/369, FILING DATE: 2002-04-02 APPLICATION NUMBER: US09/659, FILING DATE: 2000-09-12 APPLICATION NUMBER: US60/318, FILING DATE: 2001-09-07	PRIOR FILING DATE: 2002-06-19 PRIOR PILING DATE: 2000-08-10 PRIOR PILING DATE: 2000-08-10 PRIOR PILING DATE: 2000-08-10 PRIOR PILING DATE: 2001-09-12 PRIOR FILING DATE: 2001-09-12 PRIOR PILING DATE: 2002-05-13 PRIOR PILING DATE: 2002-05-15 PRIOR PILING DATE: 2002-05-15 PRIOR PILING DATE: 2002-05-15	APPLICANT: Shinkets, Richard A  APPLICANT: Smithson, Glennda  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME  FILE REFERENCE: 21402-442A  CURRENT APPLICATION NUMBER: US/10/236,392  CURRENT FILING DATE: 2002-09-06  PRIOR APPLICATION NUMBER: US09/540,763  PRIOR FILING DATE: 2000-03-00  PRIOR FILING DATE: 1000-03-00  PRIOR FILING DATE: 2000-03-00	miller, Ch millet, Ch Padigaru, Patturajan Panta, Caro Pennan, Jo Rastelli, Rastger, Da Ratenberg Shenoy, Su	***********	
Db 316 yrGlyGlyAsnLeuAsnGlyGluProCysValleuProPheThrTyrAsnGlyArgThrP 336  Qy 745 AGCAAGGCTTAAGTCCAAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATA 804  Db 336 heTyrSerCysThrThrGluGlyArgGln	640 TGGTTGGTTAGCGTTGGTGGAGGGGAGCGAATCAAGACATTAGGTCTTAAATTTT :::::::::::::::::::::::::::::	259 yrGlnProGlnProHisProGlnProProProTyrGlyHisCysValThrAspSerGlyV  594	Qy  4/8 ACCIGCTCCAGICACAGCAACGGCCAAGGAGAGTGIGAGAGGACACA 537  Qy  538 CCTCTGTGCAGACCACTGCACGGCCCAGGAGAGTGIGAGAGGACACA 537  Qy  538 CCTCTGTGCAGACCACATCGAGCGGATCTGACCGATGTTCGTATTGCT 593	369GAAGGCAGCGAGCGATCACTTGCACTTCTAGAAATAGATGCAACGATCACTTGCACTTCTAGAAATAGATGCAACGATCACTTGCACCTTCTAGAAATAGATGCAACGATCACTTGCACCTTGCACCTTGCACCTAGAAATAGATGCAACGATCACTTGCACGACGATGCAACGATGCAAGAATGGAAATAGATGGAAGAATAGATGGAAGAATAGAAGA	Db 126 -GlyĠİyTyrMetLeuĠİuCysValCysLeuĠlyAsnGlyLysGlyĠİu-TrpThr 143  Qy 284 TGCAAGCACAACAGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGGGACTT 343  Db 144CysLysProIleAlaGluLysCysPheAspHisAlaAlaGlyThrS 159  Qy 344 CCTATGTGGTCGGAGAAACGTGGGA 368	Qy 107 CCGCCAGCCTAGCCGGGTCCTCAACGACAGAGCACGATCATGCGCACCCGTGGCCAGGA 166  Db 122 oHisGluThr	Query Match:       17.07%       Indels:       326         DB:       4       Gaps:       23         US-09-940-235-12 (1-2096) x US-10-236-392-2 (1-2320)       US-09-940-235-12 (1-2096) x US-10-236-392-2 (1-2320)         Qy       5       GACCATTCATGTTGTTGCTCAGGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG

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AGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAA 1983
                                 CTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATC 1923
                                                                                                                        CCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTA 1863
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 64
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoereh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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                                        CAACGGTTTCCCTCTAGAA---ATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGG 283
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                                                                                                                                                                                                                                                                                                                                                                                            GACCATTCATGTTGCTCAGGTCGCAGACGTTTTGCAGCAGCAGTCGCTTCACGT---
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Kamatkar, Shubhangi
Glatt, Karen
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1224	CCATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAG 1	1165
393		393
1164	ACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACA 1	1105
393		393
1104	ACCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATG 1	1045
393		393
1044	TTAGACCATATAAAGAAAAACCAATACAAA	985
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984	a	925
924 382	GTAACGACGACTACTTTGAGGTCATTGATTTTTGCAAGCGATGCAACCATTACTGATCGAA (	363
363		354
864	AACGTCCACA	805
353	heTyrSerCysThrThrGluGlyArgGln	344
804		745
4.	:::    :::    OPheThrTyrAsnGlyArgThrP	324
744	TTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAG	700
N	:::: etLeuCysThrCysLeuGlyAsnGlyValSerCysGlnGluThrAlaValThrGlnThrT	0
699	TGGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTT	640
639		287
OD.	yrGlnProGlnProHlsProGlnProProProTyrGlyHisCysValThrAspSerGlyV	ວ ດ
593		•
267	hrSerValGlnThrThrSerSerGlySerGlyProPheThrAspValArgAlaAlaValT	4
593	CCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTATTGCT	538
537 247	ACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGTGGAAGTGTGAGAGGCACACACTGCTGAGAGGCACACACTGCAGAGTGGAGAGTGGAGAGGCACACACA	227
227	lnAspThrArgThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyA	0
477	AGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAA	418
207	hrCysLeuGlyGluGlySerGlyArgIleThrCysThrSerArgAsnArgCysAsnAspG	<b>6</b> 0
- 1	GAAGGCAGCGCATGCATTGCATTTGCATTTTAGAAATAAGATGCAATGCAATGCAATGCATGC	369
368 187	CCTATGTGGTCGGAGAAACGTGGGA	344 167
167		152
343	TGCAAGCACAACAGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTT	284

2044 CCTCTGTGCAGACCACATCGAGCGGATCTGGCCCC 2078		B 8
556 alArgTyrGlnCysTyrCysTyrGlyArgGlyIleGlyGluTrpHisCysGln 573		밁
1984 ACCTGCTCCAGTGCATCTGCACAGGCAACGGCAGGAGAGTGGAAGTGTGAGAGGCACA 2043		ð
1924 AGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAA 1983 :::		음 성
517 hrCysPheGlyGlnGlyArgGlyArgTrpLysCysAspProValAspGlnCysGlnAspS 537		문
1864 CTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATC 1923	Qy 18	0
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1804 CCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTA 1863	Qy 18	ю
479 rpThrCysIleAlaTyrSerGlnLeuArgAspGlnCysIleValAspAspIleT 497		문
1750 CGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTT 1803	17	۵
	Db 4	U
1690 ATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGCTACCATTTAGCTGGTGGTGGCCAGG 1749	Qy 16	ю
451 yrArgIleGlyAspGlnTrpAspLysGlnHisAspMetGlyHisMetMetArgCysThrC 471	Db 4	0
1630 ATACCTTAACTGGAAAAGTAGAGGATAATCACGATGACACCCAACCGTATCATAACCGTTT 1689	Oy 16	ю
448GlyValMetT 451	Db 4	ы
1570 ATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTTGGTATTATGGACT 1629	Оу 15	o
437 laAlaHisGluGluIleCysThrThrAsnGlu 447	Db .	מ
1510 TAAAAAGTGAGCTCTTAACAGCTAGCGAACGTAACTTAGACTTCAGAGATTTATACG 1569	Qy 1:	0
417 ysTrpCysGlyThrThrGlnAsnTyrAspAlaAspGlnLysPheGlyPheCysProMetA 437	Db 4	н
1465 AACTGTTCACCATCAAATACGTTGATGTCGATACCAACGAATTGC 1509	0y 1,	0
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1405 AATATTACGTCCTTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGA 1464	ř. Š	0
402His-AsnTyrThrAspCysThrSerGluG 411	Db .	н
1345 GGATCAATAAAAATCTGGTCTGAATGAAGAAAATAAACAACACTGACCTGATCTCTGAGA 1404	1:	0
397 eLeuTyrAsnAsn 401	DЬ	ш
1285 CGATTTTACCAATGGATCAAGAGTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATA 1344	Qy 1:	0
394HisPheProPh 397	Db .:	н
1225 GCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTTCCGTA 1284	Qy 1:	_

Search completed: January 28, 2006, 02:58:03 Job time : 186.069 secs

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Result
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-Q=/cgn2 1/USFTC | D/US09940235/runat 27012006 144220 27676/app query.fasta 1.7708 |
-DB=Published | Applications | April | New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1 |
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 |
-TRANUS=hunan40.cdi -LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 |
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 |
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 |
-FGAPDOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2006
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US-11-032-951-12

US-10-995-561-622

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US-10-995-561-627

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US-10-995-561-626
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Sequence 2, Appli
Sequence 622, App
Sequence 629, App
Sequence 629, App
Sequence 623, App
Sequence 623, App
Sequence 627, App
Sequence 626, App
Sequence 4, Appli
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US-11-128-059-82	-11-128-059-7	-11-128-059-	-10-485-517-13	-10-453-372-11	-10-453-372-114	-11-013-759-1	-10-485-517-	-11-016-564-	0-055-877-1	-10-055-87	-11-124-368A-	-11-174-1	-10-793-626-	-11-032-951-	-11-115-6	-11-115-639-	-11-115-639-3	-11-052-554A	-10-485-517-319	-11-052-554A-	-11-052-5	-11-013-759-	-11-013-759-	-11-013-7	-11-013-759-	-10-995-561-63	0-995-561-62	-10-995-561-62	-10-995-561-62	-10-995-561-63	-10-995-561-63	-10-995-561-6	-10-995-561-63	1-006-119-3
82,		60,	e 131	e L	114	e 11,	212	equence 5,	equence 141	equence 140	equence 292	e 29,	equence 960,	equence 7,	equence	32	ŭ	26	Sequence 319, App	17	8	equence 7,	equence 4,	equence 13	equence 3,	equence 63	e 621	equence 62!	equence 62	equence 63	equence 63:	equence 62:	equence	ш

## ALIGNMENTS

US-10-631-558-2

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Sequence 2, Application US/10631558
Publication No. US2005020598A1
GENERAL INFORMATION:
APPLICANT: ROY, Chait
APPLICANT: Sahni, Girish
APPLICANT: Roy, Chait
APPLICANT: Rajagopal, Kammara
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Vadav, Mahavir
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 07064-009002
CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT APPLICATION NUMBER: US/9940,235
PRIOR APPLICATION NUMBER: US/9940,235
PRIOR APPLICATION NUMBER: US/99940,235
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
CURCENT: Streptococcus equisimilis
US-10-631-558-2
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Alignment Scores:

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                                                                                                                      SerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu
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APPLICANT: KANGALOW.

APPLICANT: Rabkin, Simon W.

TITLE OF INVENTION: Peptides and Their Use to Title OF INVENTION: Cell Death

FILE REFERENCE: 50216/003005

CURRENT APPLICATION NUMBER: US/11/032,951

CURRENT FILING DATE: 2005-01-11

PRIOR APPLICATION NUMBER: US 09/919,703

PRIOR FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 09/294,457

PRIOR FILING DATE: 1999-04-19

PRIOR APPLICATION NUMBER: US 09/59,599

PRIOR APPLICATION NUMBER: US 60/008,233

PRIOR APPLICATION NUMBER: US 60/008,233

PRIOR FILING DATE: 1995-12-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12
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US-11-032-951-12
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: US-11-032-951-12
                                                                                                                                                                                                                                                                        US-09-940-235-12 (1-2096) x US-11-032-951-12 (1-413)
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                             LysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeu
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RESULT 3

US-10-95-561-622

; Sequence 622, Application US/10995561

; Publication No. US20050272054A1
  GENERAL INFORMATION:
APPLICANT: CARCILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CERDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 622
LENGTH: 657
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-622
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Alignment Scores: Pred. No.:  634.50  Score:  Score: Percent Similarity: 36.69% Best Local Similarity: 17.03% Dest Local Simil	Db 496 ysThrCysValGlyAsn

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N'ENTION: DETECTION AND USES THEREOF NCE: CL001559 LICATION NUMBER: US/10/995,561	; APPLICANT: CARGILL, Michele et al. ; APPLICANT: CARGILL, Michele et al. ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF	US-10-95-561-633 US-10-95-561-633, Application US/10995561 ; Sequence 633, Application US/1099561 ; Publication No. US20050272054A1 ; GRNERAL, INFORMATION.	2 1 1			QY 1858 ATTGEMENTECCTGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	522	504		477	475 1624		Db 442 snMetLysTrpCysGlyThrThrGlnAsnTyrAspAlaAspGlnLysPheGlyPheCysP 462  Ov 1504 AATTGCTAAAAAGTGAGCAGCTTTAACAGCTTAGCGAACGTTAGCATTTTAGAGAGTTT 1563		Db 430	1279 TCCGTAGGATTTTACCAATGGATCAAGAGTTTACTTACCGTGTTAAAAATCGGGAACAAG	1219 ACCCAGGCTATACGATTTATGAACGTGACTCCCCAATGATCACCAATGACAATGACAATTT  413GlyAsnSerAsnGlyAlaLeuCysHis  1270 MCCCTACGATTTTAGGAACGCATGAGAACGCTTTTTTAGGATGAGAACGATTTT  1270 MCCCTACGATTTTAGGAACGCATGAGACGCTTTTAGGATGATGAGAACACTTTTTAGGATGAGAACACTTTTAGGATGAGAACACTTTTAGGATGAGAACACTTTTAGGATGAGAACACTTTTAGGATGAGAACACTTTTAGGATGAGAACACTTTTAGGATGAGAACACTTTTAGGATGAGAACACTTTTAGGATGAGAACACTTTTAGAGAACACTTTTAGAGATGAGAACACTTTTAGAGAACACTTTTAGAGAACACTTTTAGAACACTTTTAGAGAACACTTTTAGAGAACACTTTTAGAGAACACTTTTAGAGAACACTTTTAGACAATAAATA	407LeuValGlnThrArgGly

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Qy 227 CAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGG 283	Db 160 160	QY 167 CCCAACGCTGCCCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCA 226	157 OHisGluThr	CACTACION CONTROLO ACCIONACION CONTROLO ACCA	Db 142 HisGluGlyGlyGlnSerTyr-LysIleGlyAspThrTzpArgArgPr 157	0.7 C C C C C C C C C C C C C C C C C C C	Qy 5 GACCATTCATGTTGCTCAGGTCGCAGACGTTTTGCAGCAGCAGCAGCAGCCGTTCACGT 61	US-09-940-235-12 (1-2096) x US-10-995-561-623 (1-2355)	Indels: Gaps:	nt Similarity: 36.69% Local Similarity: 27.42%	7.: 2.48e-40 Length: 634.50 Matches:			LENGTH:	SEQ for	CURRENT FILING DATE: 2004-11-24  : NUMBER OF SEO ID NOS: 85702	FILE REPERENCE: CLOO1559		CANT: CARGILL,	; Sequence 623, Application US/10995561 Publication No. US20050272054A1	RESULT 6 US-10-995-561-623		ACATCG	582	ов плануватоверского представление под под под под под под под под под под	CAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATC 1	542	TGTACTTGCCTGGGAGAAGGCAGCGGACGCATC	::::        :::        ::::	GGACTTCCTATGTGGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGTTAG 1	\text{Vy}  1/44  \text{GCCGAGAGTTTTTGATCATGCTGCTG} 1797	
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RESULT 7

US-10-995-561-627
; Sequence 627, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
GENERAL INFORMATION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOUSE9
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
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SOFTWARE: FASTSRQ for Windows Version
SEQ ID NO 627
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TYPE: PRT
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                                                                 alValTyrSerValGlyMetGlnTrpLeu------LysThrGlnGlyAsnLysGlnM 331
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Qy 62TCGCTCGCGTATCGGTGATTCATTCTGCTAACCAGTAAGGCAACC 106	7 1564 TATACGATICCTUGTGATAAGGCTAAACTACTCTACAACAATCTCGGATGCTTTTGGTATTA 1623 5 475Glydalm 477	문 성
151 AspCysThrCysIleGlyAlaGlyArgGlyArgIleSerCysThrIleAlaAsnArgCys	462 rometAlaAlaHi8GluGluIleCysThrThrAshGlu	}
5 GACCATTCATGTTGTTGCTCAGGTCGCAGACGTTTTTGCAGCAGCAGCAGTCGCTTCACGT	1504 AATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAACTTCAGAGATT	}
US-09-940-235-12 (1-2096) x US-10-821-234-1545 (1-2384)	442	뫄
6 Gaps:	Y 1459 ACTTGAAACTGTTCACCATCAAATACGTTGATGTCGATACCAACG 1503	Ş
Local Similarity: 27.42% Mismatches:  Match: 17 03% Todolo.	436 erGluGlyArgArgAspA 442	밁
: 2.48e-40 634.50	Y 1399 CTGAGAAATATTACGTCCTTAAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTC 1458	Ş
ment Scores:	430AsnTyrThrAspCysThrS 436	뮍
) OKGANISM: HOMO BADIENS US-10-821-234-1545	Y 1339 CTTATAGGATCAATAAAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCT 1398	Ş
TYPE: PRT	0 422 429	밁
6	Y 1279 TCCGTACGATTTTACCAATGGATCAAGAGTTTACCTTACCGTGTTAAAAATCGGGAACAAG 1338	Ş
OF SEQ ID NOS: 1704	5 413 421	맑
; CURRENT FILLING DATE: 2004-04-07 ; PRIOR APPLICATION NUMBER: US 60/462,047	1219 ACCCAGGCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTT 1278	Ş
; CURRENT APPLICATION NUMBER: US/10/821, 234	b 407 412	뮰
; APPLICANT: Tang, Y. Tom ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia	1159 GTGACACCATCACATCTCAAGAATTACTAGCTCAAGCAC	ð
; APPLICANT: Stache-Crain, Birgit ; APPLICANT: Andarmani, Susan	406 406	뫄
N: Ivan	Y 1099 CTGATGACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCG 1158	S
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RESULT 8 US-10-821-234-1545	1039 TAÇAAAACÇAAGCGAAATÇTGTTGATGTGGAATATAÇTGTACAGTTTACTCCCTTAAACC	Ş
Db 601ProLeuGlnThrTyrProSerSerSerGlyPro 611	390	뮍
Qy 2038 GGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCC 2078	979 CTGTCCAAGAATTTTTGCTAAGCGGACATGTGCGCGTTAGACCATATAAAGAAAAACCAA	Ş
Db 582GlyValArgTyrGlnCysTyrCysTyrGlyArgGlyIleGlyGluTrpHisCysGln- 600		문 4
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522 spileThrTyrAsnValAsnAspThrPheHisLysArgHisGluGluGlyHisMetLeuA	341	밁
Qy 1798 GGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAAGCCCTACCAAGGCTGGATGATGGTAG 1857	760 CAAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTG	S
TrpThrCysIleAlaTyrSerGlnLeuArg	338AsnGlyValSer-	뮹
Qy 1744 GCCAGGCGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGCTG 1797	y 700 TTGAAATCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTC 759	§

1039 TAGAAAACGAAATCTGTTGATGTGGAATATACTGTACAGTTTACTCCCCTTAAACC 1098	CCTATGTGGTCGGAGAAACGTGGGA	227 CAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGG 283     :::
RESULT 9  (US-10-995-561-626 (Sequence 626, Application US/10995561 (Publication No. US20050272054A1 (Publication No. US20050272054A1 (Publication No. US20050272054A1 (PUBLICANT: CARGILL, Michele et al. (APPLICANT: CARGILL, Michele et al. (TITLE OF INVENTION: CENETIC POLYMORPHISMS ASSOCIATED WITH (TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF (TITLE OF INVENTION: DETECTION AND USES THEREOF (PILE REFERENCE: CL001559	OW 1279 TOOGRACGATTTACCAATGATCAAGAGTTTACTTACGGGAACAAG 1338  A51	436

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Best Local Similarity:
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 626
LENGTH: 2386 :
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                        alValTyrSerValGlyMetGlnTrpLeu-----LysThrGlnGlyAsnLysGlnM
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                                                                                yrGlnProGlnProHisProGlnProProProTyrGlyHisCysValThrAspSerGlyV
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                                                                                                                                                                          AATTGCTAAAAAGTGAGCAGCTCTTAACAGCTAGCGAACGTAACTTAGACTTCAGAGATT 1563
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                                                                                                                        TATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAATCTCGATGCTTTTGGTATTA 1623
                                                                                                                                                roMetAlaAlaHisGluGluIleCysThrThrAsnGlu------ 474
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                                                                                                                                                                                                                                                       -----ArgArgAspA 442
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                              US-09-940-235-12 (1-2096) x US-10-631-558-4 (1-259)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/631,558
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-631-558-4
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Publication No. US20050260598A1
GENERAL INFORMATION:
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APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
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APPLICANT: Sahni, Giris
APPLICANT: Roy, Chait
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                      1698 AAGCGACCCGAAGGAGAGAATGCTAGCTACCATTTA------GCTGGTGGTGGTCGC 1745
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                       ArgArgProHis---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGly 142
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                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: US 60/527,153
PRIOR FILING DATE: 2003-12-05
PRIOR APPLICATION NUMBER: US 60/565,093
PRIOR FILING DATE: 2004-04-22
PRIOR PPLICATION NUMBER: US 60/625,519
PRIOR PILING DATE: 2004-11-06
PRIOR FILING DATE: 2004-11-06
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 31
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APPLICANT: Ward,
APPLICANT: Caffr
APPLICANT: Spith
APPLICANT: Li, H
APPLICANT: Podue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Appropriate Publication No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Li, Hongshan
APPLICANT: Podust, Vladimir
APPLICANT: Perichon, Regis
APPLICANT: Ciphergen Biosystems, Inc.
TITLE OF INVENTION: Serum Biomarkers for Chagas
FILE REFERENCE: 016866-012130US
                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: N-terminal 28.7 fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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1746 CAGGCGCAA---CAGATTGTACCCATAGCTGAGAAGTGTTTTGATCATGCTGCGGGACT 1802
                                                                                                              1698 AAGCGACCCGAAGGAGAGATGCTAGCTACCATTTA-----GCTGGTGGTGGC 1745
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                                                                    124 ArgArgProHis---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGly
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Spithill, Terry
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GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPON

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 631

LENGTH: 642
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Query Match:
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AACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAAGTGTGAGAGGCAC 2042
                     ACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGAT
                                                                                                                     SerTyrValValGlyGluThrTrpGluLy8ProTyrGlnGlyTrpMetMetValAspCys
                                                                                                                                TCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGT
                                                                                                                                                                                                                   ArgArgProHis---GluThrGlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGly
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LENGTH: 1341
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Percent Similarity:
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Query Match:
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Publication No. US20-
GENERAL INFORMATION:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRU
TITLE OF INVENTION: DETECTION AND USES THEREOF
TILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 632

LENGTH: 693
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Query Match:
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US-10-995-561-632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-995-561-632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 632, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1239 lyGluPheLysCysAspProHis 1246
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                         706 TCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAG---CAAGGCTTAAGTCCAA 762
                                                                                                                                                646 TTAGCGTTGCTGGTACTGTTGAGGGGGACGAATCAAGACATTAGTCTTAAATTTTTTTGAAA 705
                                                                                                                                                                                                   132 snLeuAla----
                                                                                                                                                                                                                                                                                              112 u-ThrGlyTyrArgValArgValThrProLysGluLysThrGlyProMetLysGluIleA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 GATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 TATGTGGTCGGAGAAACGTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATA 405
                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TyrValValSerValTyrAlaGlnAsnProSerGlyGluSerGlnProLeuValGlnThr 80
spThrLeuThrSerArgProAlaGlnGlyValValThrThrLeuGluAsnValSerProP 180
                                                                                            alSer-----GlyLeuMetValAlaThrLysTyrGluValSerValTyrAlaLeuLysA 160
                                                                                                                                                                                                                                               GTATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTG 645
                                                                                                                                                                                                                                                                                                                                                 GTGAGAGGCACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTC 585
                                                                                                                                                                                                                                                                                                                                                                                                PheThrGlnValThrProThrSerLeuSerAlaGlnTrpThr-ProProAsnValGlnLe 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCCAACGGCCGAGGAGAGTGGAAGT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGAGTGGAAGTGTGAGAGGCAC 2042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpAspArgGlnGlyGluAsnGlyGlnMetMetSerCysThrCysLeuGlyAsnGlyLysG 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10995561
o. US20050272054A1
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	1591 TACTCTACAACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACTGGA 1643
B :	447 lyThrAspGluGluProLeuGlnPheArgValProGlyThrSerThrSerA 464
o !	1531 CAGCTAGCGAACGTAACCTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAAC 1590
Db 49	427 hrileSerTrpAlaProPheGlnAspThrSerGluTyrIleIleSerCysHisProValG 447
0 0	1474 CCATCAAATACGTTGATGTCGATACCAACGAATTGCTAAAAAAGTGAGCAGCTCTTAA 1530
Query DB:	1428GAAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAAACTGTTCA 1473
Perce	lnMetIlePh
Pred	1427 1427
US-10	 367 spThrGlyAsnGlyIleGlnLeuProGlyThrSerGlyGlnGlnProSerValGlyGlnG 387
	1414 TCCTTAAAAAAGGG 1427
SES	1362GTTCTGAATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTACG 1413
 3 O E	1306 AGTTTACTTACCGTGTTAAAAATCGGGGAACAAGCTTATAGGATCAATAAAAAATCT 1361   :::                :::     :::
 3 > B	1291 TACCAATGGATCAA
US-10 ; Sec ; Pul	1234 TTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTT 1290
Db RESU	1197GAJAGCATTTTAAACAAAAACCACCCA
& B	 
SS.	TACTAGCTCAAGCA
₽ \$	ATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAAT
Db Db	228 alArgSerTyrThrIleThrGlyLeuGlnProGlyThrAspTyrLys 243
	1063 ATGTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTC 1122
Db	1003 GACATGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGTTG 1062
0 1	196SerTrpArgThrLysThrGluThrIleThrGlyPheGlnValAspA 211
P 5	943 CTGACAAAGATGGTTCGGTAACCTTGCCGACCCAACCTGTCCAAGAATTTTTTGCTAAGCG 1002
⊋ b	::::::          188AlaThrGluThrThrIleThrIle 195
Qy	AGGTCATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTTG
рь	
Q	TACTAAAGGCTATTCAAGAAACAATTGATCGCTAAACGTCACAGAGGACGACGACTGACT
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BENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
APPLICANTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
                                                                                                                                                                                                                                                                 cent Similarity:
t Local Similarity:
ry Match:
                                                                                                                                                                                             )9-940-235-12 (1-2096) x US-10-995-561-630 (1-1315)
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SOFTWARE: FastSEQ for Windows Version 4.0
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Ablication No. US20050272054A1
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10-995-561-630
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                                                                                                                                                                                                                                                                                                                                                                                                                                             0-995-561-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1729 ATTTAGCTGGTGGCCAGGCGCAACAGATTGTACCCATAGCTGAGAAGTGTTTTGATC 1788
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                                               406
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                                                                                                                                             346 TATGTGGTCGGAGAAACGTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          594 yeCysAspProHis 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536 heLysLeuCysGlnCysLeuGlyPheGlySerGlyHisPheArgCysAspSerSerA 556
703 AlavalThr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 rgGlyAlaThrTyrAsnIleIleValGluAlaLeuLysAspGlnGlnArgHisLysValA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 la---
                                               GATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGG 465
                                                                                               TyrVaiValSerValTyrAlaGlnAsnProSerGlyGluSerGlnProLeuValGlnThr 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGA 2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGA 1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGA 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgTrpCysHisAspAsnGly-----ValAsnTyrLysIleGlyGluLysTrpAspArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roTyrThrValSerHisTyrAlaValGlyAspGluTrpGluArgMetSerGluSerGlyP 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rgGluGluValValThrValGlyAsnSerValAsn---GluGlyLeuAsnGln----- 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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----ThrIleProAlaProThrAspLeuLys 714
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1427	1414 TCCTTAAAAAAGGG	
rA 989	969 roLeuIleGlyArgLysTyrThrValGlnLysThrProPheValThrHisProGlyTyrA	٠
	953 luTyrThr	
13	1306 AGTTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAATCT	1
-G 1305     953	1291 TACCAATGAATCAA	ц
TT 1290	1234 TTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGAT	_
GA 1233    eI 920	1197CAAAGCATTTTAAACAAAAACCACCCAGGCTATACGA	<u>,</u>
T 900	880 alValileAspAlaSerThrAlaIleAspAlaProSerAsnLeuArgPheLeuAlaThrT	
1196	1183 TACTAGCTCAAGCA	_
088 AO	866IleTyrLeuTyrThrLeuAsnAspAsnAlaArgSerSerProV	
AT 1182	1123 TCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGA	μ.
	850 alArgSerTyrThrIleThrGlyLeuGlnProGlyThrAspTyrLys	
TC 1122	1063 ATGTGGAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGG	_
₽V 850	:::	
TG 1062	1003 GACATGTGCGCGTTAGACCATATAAAGAAAAACCAATACAAAACCAAGCGAAATCTGT	سو
pA 833	::: :::     :::          ::: :::       :::       :::	
CG 1002	943 CTGACAAAGATGGTTCGGTAACCTTGCCGACCCGACCTGTCCAAGAATTTTTGCTAAG	
817	810AlaThrGluThrThrIleThrIle	
TG 942	883 AGGTCATTGATTTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTT	
809	809	
TG 882	823 TACTAAAGGCTATTCAAGAACAATTGATCGCTAACGTCCACAGTAACGACGACTACTTTG	
809	802 roArgArgAlaArgValThrAsp	
CT 822	763 AATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAGCTGA	
OP 802	782 spThrLeuThrSerArgProAlaGlnGlyValValThrThrLeuGluAsnValSerProP	
AA 762	706 TCGATCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCC	
AA 705 : sA 782	646 TIAGCGTTGCTGGTACAGTTAGATCTAAATTTTTTTGAAA	
	, ,	
TG 645	586 GTATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTG	
eA 754	734 u-ThrGlyTyrArgValArgValThrProLysGluLysThrGlyProMetLysGluIleA	
TC 585	526 GTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGT	
GT 525 :: Le 734	466 ATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGT :::	

989 spThrclyAssnGlyIlegInLeuProGlyThrSerGlyGlnGlnProSerValGlyGlnG 1009 1427

Search completed: January 28, 2006, 02:58:49 Job time : 44.0689 secs

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-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09940235 @CGN_1_1_185 @runat 27012006 144218 27578 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=6
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Perfect score:
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Maximum Match 10
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12
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                               1984
1951.5
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Match
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## ALIGNMENTS

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Best Local Similarity:
Query Match: US-09-940-235-12 (1-2096) x A22801 (1-440) C; Superfamily: streptokinase A;Residues: 1-440 <MAL>
A;Cross-references: UNIPROT:P00779; Score: Alignment Scores: A;Experimental source: strain H46A A; Molecule type: DNA A; Accession: A22801 Genetics: No.: 648 588 ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATTGGTTGTT 647 47 27 AGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTTTGAAAATC 707 IleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuValVal SerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeuLysPhePheGluIle 1984.00 100.00% 100.00% 53.25% 3.29e-126 UNIPARC:UPI000002BE73; GB:X72832; NID:g407876; Length: Matches: Conservative: Mismatches: Indels: 440 383 0 Streptococcus equisimilis 99 46

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R.Jackson, K.W.; Tang, J.

Biochemistry 21, 6620-6625, 1982

Biochemistry 21, 6620-6625, 1982

A;Title: Complete amino acid sequence of streptokinase and A;Reference number: A00967; MUID:83127125; PMID:6760891

A;Accession: A00967

A;Accession: A00967

A;Molecule type: protein

A;Residues: 1-415 < JAC>

A;Residues: 1-415 < JAC>

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Streptokinase G precursor - Streptococcus sp. (strain 19908) C;Species Streptococcus sp. C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004 C;Accession: S02723 #Sequence of the streptokinase gene from a group-G Streptococcus. R;Malter; F; Siegel, M.;Malke, H. Nucleic Acids Res; 17, 1262, 1989 A;Title: Nucleotide sequence of the streptokinase gene from a group-G Streptococcus. A;Reference number: S02723; MUID:89160265; PMID:2922269 A;Reference number: S02723; MUID:89160265; PMID:2922269 A;Rolecule type: DNA A;Residues: 1-440 {ANL> A;Residues: 1-440 {ANL> A;Residues: 1-440 {ANL> A;Residues: 1-440 {ANL> A;Coses-references: UNIPROT:P10519; UNIPARC:UPI000013614B; EMBL:X13400; NID:947095; PIDX C;Genetics: NGC	Db 221 SerSerlleValThrHisAspAsnAspllePheArgThrIleLeuProMetAspGlmGlu 240  Qy 1308 TTTACTTACCGTGTTAAAAATCGGGAACAAGGTTAXAGGATCAATAAAAATCTGGTGTG 1367
Oy 1248 TCCTCAATCGTCACTCATGACATTTTCCCGTACGATTTTACCAATGGATCAAGAG 1307	Db 67 ASPLEUTHISETATGPTOALAHISGLYGLYLYSTHTGLUGLTGLYLEUSETPTOLYSSET 86  Qy 768 AAACCATTTGCTACTGATAGTGGGGCGATGTCACATAACTTGAGAAAGCTGACTTACTA 827

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streptokinase A precursor - Streptococcus pyogenes (strain SP130/13) (;Species: Streptococcus pyogenes C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-JiC;Accession: S02724 R;Walter, F.; Siegel, M.; Malke, H. Nucleic Acids Res. 17, 1261, 1989 #surpleic Acids Res. 17, 1261, 1989 A;Title: Nucleotide sequence of the streptokinase gene from a Streptokinase mumber: S02724; MUID:89160264; PMID:2646590 A;Accession: S02724
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A; Residues: 1-440 <WAL>
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                                                                   AspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeu
                                                                                GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA
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streptokinase - Streptococcus pyogenes C;Species: Streptococcus pyogenes C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004 C;Accession: A43867; JU0292 R;Ohkuni, H.; Todome, Y.; Suzuki, H.; Mizuse, M.; Kotani, N.; Horiuchi, K.; Infect. Immun. 60, 278-283, 1992
                                                                                                                                                                                                                                  Query
DB:
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A;Residues: 1-414 <OHK>
A;Cross-references: UNIPROT:Q57391; UNIPARC:UPI0000175C82
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Best Local Similari
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A;Note: sequence extracted from NCBI backbone
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A;Molecule type: DNA
A;Residues: 1-440 
A;Cross-references: UNIPROT:Q57391;
C;Genetics:
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Best Local Similarity:
Query Match:
DB:
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C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
C;Accession: S04168
R;Huang, T.T.; Malke, H.; Ferretti, J.J.
Mol. Microbiol. 3, 197-205, 1989
A;Title: The streptokinase gene of group A streptococci: cloning
A;Reference number: S04168; MUID:89343623; PMID:2668886
A;Accession: S04168
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TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
                                     GAATATACTGTACAGTTTACTCCCTTAAACCCCTGATGACGATTTCAGACCAGGTCTCAAA
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Qy  Qy  Qy  Qy  Qy  Db  Qy  Db  Qy  Db  Db  AFRESULT 8  FNHU  fibronect N; Alterna C; Specises C; Date: 2 C; Accessi R; Dean, L L R; Dean, L L R; Dean, L Proc. Nat A; Title:	C; Date: 01-Aug 1979 #sequence_revision 01-Sep-1979 #CEXE_Change 07-Out-2004 C; Accession: S5334 R; Shi, G.Y.; Chang, B.I.; Chen, S.M.; Mu, D.H.; Mu, H.L. Biochem, U. 304, 235-241, 1994 A; Title: Function of streptokinase fragments in plasminogen activation. A; Reference number: S5334 A; Reference mumber: S5334; MUID:95091634; PMID:7998939 A; Recession: S53334 A; Recession: S5334 A; Recession: S5334 A; Recession: S5334; MUID:95091634; PMID:7998939 A; Recession: S5334 A; Recession:	•
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Db 247 SerSerileValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu 266  Qy 1308 TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAATCTGGTCTG 1367  Db 267 PheThrTyrHisIleLysAspArgGluGlnAlaTyrLysAlaAsnSerLysThrGlyIle 286  Qy 1368 AATGAAGAATAAACAACACTGACCTGATCTCTGAGAAATATTAGGTCCTTAAAAAAGGG 1427  Db 287 GluGluLysThLASNASHTHTASpLeulIeSerGluLysTyrTyrValLeuLysLysGly 306  Qy 1428 GAAAAGCCGTATGATCCCTTTGATCCTGAGACTTACCATTCACAATAATACGTT 1487  Db 307 GluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleAsnTyrVal 326  Qy 1488 GATGTCGATTCCACGAATTGCTAAAAAGTGAGCTCTTTAACAGCTAGCGAACGTAAC 1547  Db 327 AspValAsnThLASHTTATACGATCCTCGTGAGACTTAACAGCTAGCGAACGTAAC 1547  Bb 327 AspValAsnThLASHTTATACGATCCTCGTGAAACTTACAGCTAGCGAACGTAAC 1667  Qy 1548 TTAGACTTCAGAACTTTATACGATCTCTGTAAAAAGTTAACGCTAACAATCTC 1607  Db 347 LeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeu 366  Qy 1568 GACGACCGTATTCGTATATACGGTTAACAGTTAACGGAAAGGTAATCTCTCTACAACAATCTC 1667  Db 367 AspAlasheGJyIleMetAspTyrThrLeuThrGJyLysValGGAAAAGGTAATCGCTAACGTAAC 1727  Db 368 ACCAACCGTATCATAACCGTTTATATCGGCCAACGACACGTAACTACCTTACAGGAATGCTAGCGAACGTTAC 1727  Db 367 AspAlasheGJyIleMetAspTyrThrLeuThrGJyLysValGGAAAAGGTAATCGCTAGC 1727  Db 368 ACCAACCGTATCATAACCGTTTATATATCGGCCAACGCACCGAACGGAACGTAC 1727  Db 367 AspAlasheGJyIleMetAspTyrThrLeuThrGJyLysValGGAAAAGGAAAATCCT 1727  Db 367 AspAlasheGJyIleMetAspTyrThrLeuThrGJyLysValGGAACAAGAATCCT 1727  Db 367 AspAlasheGJyIleMetAspTyrThrLeuThrGJyLysValGGAACAAGAATCCT 1727  Db 367 AspAlasheGJyIleMetAspTyrThrLeuThrGJyLysValGGAACAAATCCTTACGACTTACTTACGACCTTACTATACGTTTATATCGTTATATGGACCAACGAACAGGAAAAGGAATAATCGTTAGCTTACTATACGTTTATATGGACCAACGAACAGGAAAAGGAATAATCGTTAGGACTAGCTAG	

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A;Title: Molecular cloning and nucleotide sequence of a A;Reference number: A21011; MUID:83290929; PMID:6688418
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A;Title: Human fibronectin: cell specific alternative mRNA splicing generates
A;Reference number: A93529; MUID:84272258; PMID:6462919
                                               A; Molecule type: mRNA
A; Residues: 1594-2386 <BER>
                                                                                                                A; Accession: A90495
                                                                                                                                         A; Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with A; Reference number: A90495; MUID: 85280409; PMID: 2992573
                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1434-1537 <OL2>
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A; Residues: 973-2080; 2112-2386 < KO2>
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A;Accession: A91008
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A; Residues: 1594-1767, 'V', 1769-1783 < PAO>
A; Residues: 1594-1767, 'V', 1769-1783 < PAO>
A; Cross-references: UNIPARC: UPI000017432B; EMBL: X07718; NID: g31402
A; Note: the authors translated the codon AAC for residue 1631 as Asp
A; Note: the authors translated the codon AAC for residue 1631 as Asp
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A;Note: the authors translated the codon TTC for residue 1494 as Glu
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A;Reference number: S00848; MUID:88233940; PMID:3375063
A;Accession: S03917
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A;Title: Human fibronectin is synthesized as a pre-propolypeptide.
A;Referance number: A24476; MUID:87030890; PMID:3770189
A;Accession: A24476
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R;Gutman, A.; Yamada, K.M.; Kornblihtt, A.
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A; Residues: 1-49 < DEA>
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A; Residues: 1992-2147 < VIB>
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A;Residues: 1447-1540 <OLD>
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A; Residues: 1-14,'Q',16-38 <GUT>
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   UNIPARC:UPI000016A928; GB:M10905; NID:g182696; PIDN:AAA52462.1;
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                                       R;Garcia-Pardo, A.; Rostagno, A.; Frangione, Biochem. J. 241, 923-928, 1987
                                                                                                                                                                             A; Molecule type: protein A; Residues: 1441-1548 < PIE>
A; Title: Primary structure of human plasma fibronectin.
                                                                                                                                                                                                                                                      A; Accession: A92386
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A; Residues: 2291-2386 < KO3>
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A;Molecule type: protein
A;Residues: 291-300;551-560 <GAR2>
A;Residues: 291-300;551-560 <GAR2>
A;Residues: C91-300;551-560 <GAR2>
A;Cross-references: UNIPARC:UPI0000174336; UNIPARC:UPI0000174337
R;Griffin, C.A.; Calaycay, J.; Shively, J.S.; Smith, R.L.
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A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3532418
A;Accession: A60904
A;Cross-references: UNIFARC.VELVUUTARE A;Note: residues 1524-1527 are responsible for A: Franqione, B.
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A; Title: The cell attachment domain of fibronectin.
A; Reference number: A92386; MUID:82265604; PMID:705
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A; Residues: 616-677, 'Q', 679-703, 'PT' <CAL>
A; Cross references: UNIPARC: UPI0000174339
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A;Title: Primary structure of a DNA- and heparin-binding domain (domain A;Reference number: A23901; MUID:86008277; PMID:3900070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 293-301 <GRI>
A;Cross-references: UNIPARC:UPI0000174338
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A;Title: Further characterization of the binding of fibronectin to gelatin reveals the A;Reference number: S34791; MUID:93312001; PMID:8323285
A;Accession: S34791
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J. Biol. Chem. 258, 12670-12674, 1983
A;Title: Primary structure of human plasma
A;Reference number: A92398; MUID:84032463;
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A;Cross-references: UNIPARC:UPI000006E04C; GB:M14060; NID:g182701
R;Kornblihtt, A.R.; Vibe-Pederen, K.; Baralle, F.E.
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A;Title: Isolation and characterization of cDNA clones for human
A;Reference number: A21165; MUID:83221567; PMID:6304699
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A;Title: Isolation and characterization of cDNA clones for human liver fibronectin. A;Reference number: A22245; MUID:85231203; PMID:2989004
A;Accession: A22245
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A;Residues: 1948-2067 <UME>
A;Cross-references: UNIPARC:UPI00000046A;
A;Accession: B22245
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R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
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A;Residues: 1975-1991;2017-2039 <UM2>
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;Residues: 32-47,'C',49-51,'S',53-72,'A',74-290 <GARl>;Cross-references: UNIPARC:UPI0000174335
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F;141-179/Domain: fibronectin type I F;186-225/Domain: fibronectin type I F;308-608/Domain: fibronectin type I F;308-608/Domain: fibronectin type I F;308-342/Domain: fibronectin type I F;309-401/Domain: fibronectin type I F;470-508/Domain: fibronectin type I F;470-508/Domain: fibronectin type I F;518-555/Domain: fibronectin type I F;518-555/Domain: fibronectin type I F;518-559/Domain: fibronectin type I F;518-559/D
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A; Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1

C; Superfamily: fibronectin type I repeat homology; fibronectin type II repeat homology;

C; Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicate f; 1-26/Domain: signal sequence #status predicted <SIG>
F; 27-31/Domain: propeptide #status predicted <PRO>
F; 32-2386/Product: fibronectin #status experimental <MAT>
F; 52-272/Domain: fibronectin type I repeat homology <1F1>
F; 97-135/Domain: fibronectin type I repeat homology <1F2>
F; 97-135/Domain: fibronectin type I repeat homology <1F2>
F; 97-135/Domain: fibronectin type I repeat homology <1F2>
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A;Residues: 2071-2080;2112-2356 <GAR4>
A;Residues: 2071-2080;2112-2356 <GAR4>
C;Comment: The extra domain and connecting strand 3 are subject to developmental and tis C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
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A;Title: Human plasma fibronectin. Demonstration of structural differences between A;Reference number: S14357; MUID:91190085; PMID:2012601
A;Accession: S14357
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J. Biol. Chem. 260, 10320-10325, 1982.
A;Tille: Primary structure of human plasma fibronectin.
A;Reference number: A23891; MUID:85261459; PMID:4019516
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A;Residues: 1589-1630,'T',1722-2058
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A;Residues: 1614-1630,'T',1722-2081,2113-2244 <TRE>
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fibronectin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1988 #sequence revision 31-Dec-1988
C;Accession: A26452; B21165; A23292
R;Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Peters
Eur. J. Biochem. 161, 441-453, 1986
Complete
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primary structure of bovine
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|nThrTyrProSerSerSerGlyPro
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                                                                                                                                                                                                                                                                                  611
                                                                                                       #text_change 09-Jul-2004
  fibronectin
                                                   T.E.;
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F;1600-1870/Jomain: heparin binding <hr/>
F;1600-1882/Domain: fibronectin type III repeat homology <FN3N>
F;1692-1773/Domain: fibronectin type III repeat homology <FN3N>
F;1692-1773/Domain: fibronectin type III repeat homology <FN3N>
F;1781-1863/Domain: fibronectin type III repeat homology <FN3N>
F;1981-1863/Domain: fibronectin type III repeat homology <FN3N>
F;1982-2062/Jomain: fibronectin type III repeat homology <FN3O>
F;1985-2216/Jomain: fibronectin type I repeat homology <1F10>
F;2085-2124/Jomain: fibronectin type I repeat homology <1F11>
F;2130-2167/Jomain: fibronectin type I repeat homology <1F11>
F;2174-2209/Jomain: fibronectin type I repeat homology <1F11>
F;2174-2209/Jomain: fibronectin type I repeat homology <1F12>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status experime
F;21-47,45-56,66-94,92-104,110-138,136-48,155-184,182-94,200-229,227-339,277-304,302-7
7,2155-2167,2174-2200,2198-2209/Jisulfide bomds: #status predicted
F;399,497,511,846,976,1213,1987/Binding site: carbohydrate (Asn) (covalent) #status absent
F;1943,1944/Binding site: carbohydrate (Asn) (covalent) #status absent
F;1943,1944/Binding site: carbohydrate (Asn) (covalent) #status absent
F;2246/Disulfide bonds: interchain (to 2250) #status predicted
F;2250/Disulfide bonds: interchain (to 2246) #status predicted
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F;21-256/Domain: fibronectin type I repeat homology <1F2>
F;66-104/Domain: fibronectin type I repeat homology <1F2>
F;66-104/Domain: fibronectin type I repeat homology <1F2>
F;110-148/Domain: fibronectin type I repeat homology <1F3>
F;155-194/Domain: fibronectin type I repeat homology <1F4>
F;200-239/Domain: fibronectin type I repeat homology <1F4>
F;200-239/Domain: fibronectin type I repeat homology <1F6>
F;277-311/Domain: fibronectin type II repeat homology <1F6>
F;277-311/Domain: fibronectin type II repeat homology <2F1>
F;389-430/Domain: fibronectin type II repeat homology <2F2>
F;389-477/Domain: fibronectin type II repeat homology <1F8>
F;487-524/Domain: fibronectin type II repeat homology <1F9>
F;439-477/Domain: fibronectin type III repeat homology <1F9>
F;530-568/Domain: fibronectin type III repeat homology <FN3B>
F;688-770/Domain: fibronectin type III repeat homology <FN3B>
F;1675-5134/Domain: fibronectin type III repeat homology <FN3B>
F;1675-1046/Domain: fibronectin type III repeat homology <FN3B>
F;1675-1046/Domain: fibronectin type III repeat homology <FN3B>
F;1235-1318/Domain: fibronectin type III repeat homology <FN3B>
F;1410-1517/Domain: fibronectin type III repeat homology <FN3B>
F;1410-1517
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A;Molecule type: protein
A;Residues: 1-16, 'C', 18-20, 'S', 22-432;447-463;1367-1517;1567-1673;2062-2176, 'N', 2178-22
A;Cross-references: UNIPARC:UPI000017433E; UNIPARC:UPI000017433F; UNIPARC:UPI0000174340
C;Comment: Cys-1201 and Cys-2015 have free sulfhydryl groups
C;Comment: The plasma fibronectin molecule consists of two chains, which are connected
C;Comment: Fibronectins bind cell surfaces and various compounds including collagen, fi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aling, and maintenance of cell shape. C;Comment: Plasma fibronectin is synthesized by hepatocytes. C;Superfamily: fibronectin; fibronectin type I repeat homology; C;Keywords: acute phase; alternative splicing; collagen binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Petersen, T.E.; Thogersen, H.C.; Skorstengaard, Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983 A;Title: Partial primary structure of bovine plasm
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A; Residues: 2170-2265 < KOR>
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263 yrGlnProGlnProHi 594Gg [] 283 alValTyrSerValGl 640 TGGTTGTTAGCGTTGC :::::: 300 etLeuCysThrCysLe 700 TTGAAATCGATCTAAC 307 760 CAAAATCAAAACCATT	418 AGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAA	Qy 227 CAACGGTTTCCCTCTAGAAATAATTTTGTTTAAGAAGGAATATAACCATGG 283     :::      :::	Qy  5 GACCATTCATGTTGCTCGCTGCAGAACGTTTTGCAGCAGCAGTCGCTTCACGT61     ::    ::    ::    ::	F;2263/Binding site: phosphate (Ser) (covalent) #status experimental Alignment Scores: Pred. No.: Cover: Fred. No.: Cover
Db 444	Qy 1399 CTGAGAAATATTACGTCCTTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTC 1458	1159 376 1219 382 1279 391 1339 399	339 979 359 1039 363 1099	310

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A;Experimental source: strain ET1/M1
A;Note: allele 2:
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A;Title: Molecular population genetic analysis of the streptokinase gene of Streptococcu A;Reference number: S77671; MUID:96037795; PMID:7565111
A;Accession: S77671
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S77671
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Best Local Similarity:
Query Match:
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A;Cross-references: UNIPARC:UPI0000000562;
A;Experimental source: strain E2/M3
A;Note: allele 3
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A; Residues: 1-128 < KAP>
A; Cross-references: UNI
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                                                                                                                                                                                                                               1008 GTGCGCGTTAGACCATATAAAGAAAACCAATACAAAACCAAGCGAAATCTGTTGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1981
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     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydrolase;
                       GCTCAAGCACAAAGCATTTTAAACAAAAAACCCACCCAGGCTATACGATTTATGAACGTGAC
                                                                                      GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCCATCACATCTCAAGAATTACTA 1187
                                                                                                                                   GAATATACTGTACAGTTTACTCCCTTAAACCCTGATGACGATTTCAGACCAGGTCTCAAA 1127
                                                                                                                                                                                                        GAAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCAACGAGGAGAGTGGAAAGTGTGAGAGGGC 2040
                                                                     AspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCC 2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ysThrCysPheGlyGlnGlyArgGlyArgTrpLysCysAspProValAspGlnCysGlnA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spSerGluThrArgThrPheTyrGlnIleGlyAspSerTrp---GluLysTyrLeuGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lyValArgTyrGlnCysTyrCysTyrGlyArgGlyIleGlyGluTrpAlaCysGln----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leThrTyrAsnValAsnAspThrPheHisLysArgHisGluGluGlyHisMetLeuAsnC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasminogen
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620.00
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92.19%
16.64%
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Matches:
                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                 Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and 3) - Streptococcus pyogenes (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: U25854; NID: g818910; PIDN: AAA85730.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL:U25853; NID:g818908;
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A; Nolecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-139; 2382-2477 < PAT>
A; Cross-references: UNIPARC: UPI000017095C; UNIPARC: UPI0000177AEF;
A; Cross-references: UNIPARC: UPI000017095C; UNIPARC: UPI0000177AEF;
A; Note: the authors translated the codon CCT for residues 51 and 9
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A;Residues: 609-1810, 'T',1812-2283 <SCH>
A;Residues: 609-1810, 'T',1812-2283 <SCH>
A;Cross-references: UNIPARC: UPI0000177AEA; EMBL:X15906
A;Cross-references: UNIPARC: UPI0000177AEA; EMBL:X15906
R;Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A;Title: A single rat fibronectin gene generates three A;Reference number: A22319; MUID:84298097; PMID:6089177
A;Accession: A22319
A;Residues: 1586-1720,'T',1722,1813-2477 <SC2>
A;Cross-references: UNIPARC:UPI0000177AF0
R;Codermatt, E.; Tamkun, J.W.; Hynes
Proc. Natl. Acad. Sci. US.A. 82, 6571-6575, 1985
A;Title: Repeating modular structure of the fibronectin
A;Reference number: 159049; MUID:86016741; PMID:3863113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1183-1192;GLN',1268,'P',1270-1271,'D',1273,'CP',1276,'PY';1385-1399 <FALS
A;Cross-references: UNIPARC:UPI0000177AEC; UNIPARC:UPI0000177AED; UNIPARC:UPI0000177AEE
R;Patel, R.S.; Odermatt, B.; Schwarzbauer, J.E.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 2052-2237 <TAM>
A;Residues: 2052-2237 <TAM>
A;Cross-references: UNIPARC:UPI0000177AEB
A;Cross-references: UNIPARC:UPI0000177AEB
R;Falkenberg, C.; Enghild, J.J.; Thogersen, I.B.; Salvesen, G.; Akerstroem, B.
Biochem. J. 301, 745-751, 1994
A;Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex
A;Reference number: S46203; MUID:94330948; PMID:7519849
                                                                                                                                                                                                                                                                                                                         Cell 35, 421-431, 1983
A;Title: Three different fibronectin mRNAs arise by alternative A;Reference number: A27252; MUID:84082067; PMID:6317187
A;Accession: A27252
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S14428
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A; Residues: 1586-1720, 'T',
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F;33-24///Product: ilbronectin type I repeat homology <IFI>
F;39-8136/Domain: fibronectin type I repeat homology <IFI>
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F;142-180/Domain: fibronectin type I repeat homology <IFI>
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F;318-726/Domain: fibronectin type I repeat homology <IFI>
F;318-31/Domain: fibronectin type I repeat homology <IFI>
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F;318-35/Domain: fibronectin type II repeat homology <IFI>
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A;Residues: 1722-1810 <-
A;Cross-references: UNI
C;Genetics:
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                                                                                                                     CCGCCAGCCTAGCCGGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGGCCAGGA 166
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A;Gene: ska
C;Superfamily: streptokinase
C;Keywords: hydrolase; plasm:
                                                                                  A; Molecule type: DNA
A; Residues: 1-128 «KAP»
A; Cross-references: UNIPROT: Q54695; UNIPARC: UPI00000BD8DC;
A; Experimental source: strain ET76/M72
C; Genetics:
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S77688
Alignment Scores: Pred. No.:
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Query Match:
DB:
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A;Accession: S77680
A;Status: translation not shown
A;Status: translation not shown
A;Status: translation not shown
A;Residues: 1-128 <KAP>
A;Residues: 1-128 <KAP>
A;Cross-references: UNIPROT:Q54687; UNIPARC:UPI00000BD2D3; EMBL:U25862; NID:g818926; PIA;Experimental source: strain ET51/M17
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5.61e-30

Length:

128

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A;Creatures: 1-201 CLBs
A;Cross-references: UNIPARC:UDIO00177AE7; GB:M77820
A;Cross-references: UNIPARC:UDIO00177AE7; GB:M77820
A;Note: sequence extracted from NCBI backbone (NCBIP:77473)
C;Superfamily: fibronectin; fibronectin type I repeat homology; fibr c;Keywords: duplication; extracellular matrix; glycoprotein; heterod F;55-90/Domain: fibronectin type I repeat homology <1F1>
F;100-138/Domain: fibronectin type I repeat homology <1F2>
F;144-182/Domain: fibronectin type I repeat homology <1F5>
F;234-273/Domain: fibronectin type I repeat homology <1F5>
F;234-273/Domain: fibronectin type II repeat homology <1F7>
F;309-343/Domain: fibronectin type II repeat homology <2F1>
F;471-509/Domain: fibronectin type II repeat homology <2F2>
F;471-509/Domain: fibronectin type II repeat homology <1F9>
F;519-556/Domain: fibronectin type II repeat homology <1F9>
F;519-556/Domain: fibronectin type III repeat homology <1F9>
F;810-693/Domain: fibronectin type III repeat homology <FN3B>
F;810-891/Domain: fibronectin type III repeat homology <FN3B>
F;906-988/Domain: fibronectin type III repeat homology <FN3B>
F;106-1165/Domain: fibronectin type III repeat homology <FN3B>
F;1077/Domain: fibronectin type III repeat homology <FN3B>
F;108-1165/Domain: fibronectin type III repeat homology <FN3B>
F;106-1165/Domain: fibronectin type III repeat homology <FN3B>
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A43908
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A;Status: nucleic acid sequence not shown; not compared with A;Molecule type: mRNA
A;Residues: 1-2481 <DES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. Biol. 149, 357-369, 1992
A; Title: Identification and characterization of alternatively
A; Reference number: A43908; MUID:92111942; PMID:1730390
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Dev. Biol. 149, 3
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;Species: Xenopus laevis (African clawed frog)
;Date: 31_Dec-1993 #sequence_revision 31-Dec-1993
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57-369, 1992
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F;1448-1530/Domain: fibronectin type III repeat homology <FN3J>
F;1538-1620/Domain: fibronectin type III repeat homology <FN3K>
F;1615-1611/Region: cell attachment (R-G-D) motif
F;1632-1714/Domain: fibronectin type III repeat homology <FN3K>
F;1632-1714/Domain: fibronectin type III repeat homology <FN3M>
F;1912-1894/Domain: fibronectin type III repeat homology <FN3N>
F;1904-1985/Domain: fibronectin type III repeat homology <FN3N>
F;1993-2075/Domain: fibronectin type III repeat homology <FN3Q>
F;1993-2075/Domain: fibronectin type III repeat homology <FN3Q>
F;2390-2340/Domain: fibronectin type III repeat homology <FN3Q>
F;2301-2340/Domain: fibronectin type I repeat homology <FN1OP
F;23046-2383/Domain: fibronectin type I repeat homology <FN1OP
F;2390-2425/Domain: fibronectin type I repeat homology <FN1OP
F;2390-2425/Domain: fibronectin type I repeat homology <FN3P
F;55-81,79-90,100-128,126-138,144-172,170-182,189-218,216-228,234-263,261-273,309-336,33
2373,2371-2383,2390-2416,2414-2425/Disulfide bonds: stratus predicted
F;2463/Disulfide bonds: interchain (to 2463) #status predicted
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Ş	1128 GATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAATTACTA 1187	
DЬ	41 AspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeu 60	
Ś	1188 GCTCAAGCACAAAGCATTTTAAACAAAAAACCACCCAGGCTATACGATTTATGAACGTGAC 1247	
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Ş	1248 TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG 1307	
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Ş	1308 TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG 1367	
DЬ	101 PheThrTyrHisValLysAsnArgGluGlnAlaTyrLysAlaAsnSerLysThrGlyIle 120	
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Search completed: January 28, 2006, 02:38:18 Job time : 56:1209 secs

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-Q=/cgn2_1/USPTO_spool_p/US09940235/runat_27012006_1-14218_27563/app_query.fasta_1.7708
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR MX==100 -THR MIN=0 -ALICH=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09940235_@CGN_1 1_1359_@runat_27012006_144218_27563 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -MATIT_DSPBLOCK=100 -LOMGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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## STREQ STRP\_STREQ 21-JUL-1986 (Rel. 01, Crea 01-APR-1988 (Rel. 07, Last 10-MAY-2005 (Rel. 47, Last Screptokinase C precursor. NCBI\_TaxID=119602; Streptococcus. Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus equisimilis Name=skc; STANDARD; Last Last Created) annotation update sequence update) 440 AA

ALIGNMENTS

MEDLINE-85232082; PubMed-2989113; DOI=10.1016/0378-1119(85)90145-3; Malke H., Roe B.A., Ferretti J.J.; "Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A."; STRAIN=H46A; NUCLEOTIDE SEQUENCE.

Gene 34:357-362(1985).

Biochemistry 21:6620-6625(1982).

-!- FUNCTION: This protein is not a protease, but it activates plasminogen by complexing with it. As a potential virulence factor, it is thought to prevent the formation of effective barriers around the site of infection, thereby contributing invasiveness of the cells. MEDLINE=83127125; PubMed=6760891;
Jackson K.W., Tang J.;
"Complete amino acid sequence of streptokinase and its homology with serine proteases."; PROTEIN SEQUENCE OF 27-440

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PIR; A09967; BZSO.
PIR; A22801; A22801.
PDB; 1L4D; X-ray; C/D=38-399.
PDB; 1L4D; X-ray; B=40-173.
PDB; 1L4D; X-ray; B=27-173.
PDB; 1L4D; X-ray; B=27-173.
PDB; 1QOR; X-ray; A/B/C/D=177-314.
SMR; P00779; 38-398.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR004093; Staphylokinase.
Pfam; PPC0821; Staphylokinase.
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PRINTS; PR01753; STREPKINASE.
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RESULT 2
Q53284 STREQ PRELIMINAR
D53284;
DT 01-NOV-1996 (TrEMBLrel.
DT 01-OCT-2003 (TrEMBLrel.
DE SKC-2.
OS Streptococcus equisimil
OC Bacteria; Firmicutes; L
OC Streptococcus.
OX NCBI TaxID=119602;
RN [1]
                                                                                               TTTACTTACCGTGTTAAAAATCGGGAACAAGCTTATAGGATCAATAAAAAATCTGGTCTG
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NUCLEOTIDE SEQUENCE.

A Estrada M.P., Hernandez L., Perez A., Rodriguez P., Serrano R.,

RA Rubbera R., Pedraza A., Padron G., Antuch W., la Fuente J., et al.;

RT "High level expression of streptokinase in Escherichia coli.";

RL Biotechnology 0:1138-1142(1992).

DR EMBL; $46336; AAC60418.1; -; Genomic_DNA.

DR PDB; 1C4P; X-ray; AB/C/D=149-285.

DR SMR; Q53284; 12-372.

DR SMR; Q53284; 12-372.

DR GO; GO:0005213; F:plasminogen activator activity; IEA.

DR GO; GO:0005515; F:protein binding; IEA.

DR InterPro; IPR004093; Staphylokinase.

DR InterPro; IPR004093; Staphylokinase.

DR InterPro; IPR008124; Streptokinase.

DR Pfam; PF02821; Staphylokinase; 3.

DR PRINTS; PR01753; STREPKINASE.

SQ SEQUENCE 414 AA; 47254 MW; F75BE5831B766904 CRC64;
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SerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGlu
             TCCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTACCAATGGATCAAGAG
                                          GCTCAAGCACAAAGCATTTTAAACAAAAACCACCCAGGCTATACGATTTATGAACGTGAC
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Costa C.S., Torres F.A.G., Filho S.A.;
Costa C.S., Torres F.A.G., Filho S.A.;
Submitted (AUG-2003) to the EMBL/GenBank/D
EMBL; AY368335; AAQ73571.1; -; Genomic_DNA
SMR; QGUK57; 59-394.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator ac
GO; GO:0008515; F:protein binding; IEA.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR004093; Streptokinase.
InterPro; IPR008124; Streptokinase.
Pfam; PF02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
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PIR; S02723; S02723.
HSSP; P00779; 1QQR.
SMR; P10519; 63-398.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR008124; Streptokinase.
Pfam; PF02821; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
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WIDLINE-89160265; PubMed=2922269;

Walter F., Siegel M., Malke H.;

"Nucleotide sequence of the streptokinase gene from a group-G
Streptococcus.";

Nucleic Acids Res. 17:1262-1262(1989).

-!- FUNCTION: This protein is not a protease, but it activates
plasminogen by complexing with it. As a potential virulence
factor, it is thought to prevent the formation of effective
barriers around the site of infection, thereby contributing
invasiveness of the cells.
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Bacteria; Firmicutes; Lactobacil
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01-JUL-1989 (Rel. 11, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasminogen activation; Signal; Virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s Swiss-Prot entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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J. Bacteriol. 186:110-121(2004).

EMBL; AYZ34137; AAP39957.1; -; Genomic_DNA HSSP; Q53284; 1C4P.

GO; GO:0016301; F: kinase activity; IEA.
GO; GO:0016301; F: kinase activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator activator ac
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Name=ska;
Streptococcus pyogenes.
Bacteria; Firmicutes; Lac
Streptococcus.
NCBI TaxID=1314;
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PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;

KALIA A., Bessen D.E.;

"Natural selection and evolution of streptococcal viru
involved in tissue-specific adaptations.";

J. Bacteriol. 186:110-121(2004).

**RMEL; AY234129, AAP39949.1; -; Genomic_DNA.

**RMEL; AY234129, AAP39949.1; -; Genomic_DNA.

**SWE, Q73078; 63-398.

SWE, Q73078; 63-398.

GO; GO:00016301; F:kinase activity; IEA.

GO; GO:0008243; F:plasminogen activator activity; IEA.

GO; GO:0005515; F:protein binding; IEA.
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01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
Streptochinase.
Name=ska;
Streptococcus pyogenes.
Bacteria; Firmicutes; Lacto
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NCBI_TaxID=1314;
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                                                      large-scale year-
into phage evolution.";
Genome Res. 13:1042-1055(2003).
Genomic Res. 13:1042-1055(2003).

ZEMBL; AE014169; AAM80305.1; -; Genomic DNA.
REMBL; BA000034; BAC64795.1; -; Genomic DNA.
REMBL; BA000034; BAC64795.1; -; Genomic DNA.
REMBL; BA000034; BAC64795.1; -; Genomic DNA.
REMBL; BA000034; F:kinase activity; IEA.
REMBL; GO; GO:0015301; F:kinase activity; IEA.
REMBL; GO; GO:001531; F:plasminogen activator activ
REMBL; GO; GO:001531; F:protein binding; IEA.
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DR InterPro; IPR008124; Streptokinase.
DR InterPro; IPR008124; Streptokinase.
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NUCLEOTIDE SEQUENCE.

STRAIN=MGAS315 / Serotype M3;

STRAIN=MGAS315 / Serotype M3;

MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;

Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.E., Parkins Mammarella N.D., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.;

"Genome sequence of a serotype M3 strain of group A Streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence" of a serotype M3 strain of group A streptocon "Genome sequence"
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01-OCT-2002 (TrEMBLrel. 2
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MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyas
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes
large-scale genomic rearrangement in invasive strains and
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Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                               Pfam; PF02821; Staphylokinase; PRINTS; PR01753; STREPKINASE.
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"Complete genome sequence of an M1 strain of Streptococcus pyoge Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
-!- FUNCTION: This protein is not a protease, but it activates plasminogen by complexing with it. As a potential virulence factor, it is thought to prevent the formation of effective barriers around the site of infection, thereby contributing invasiveness of the cells.
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MEDLINE=89160264; PubMed=2646590;
Walter F., Siegel M., Malke H.;
"Nucleotide sequence of the streptokinase pyogenes type 1 strain.";
Nucleic Acids Res. 17:1261-1261(1989).
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Streptokinase A precursor.
Name=ska; OrderedLocusNames=SPy1979;
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PubMed=14679231; DOI=10.1128/JB.186.1.110-121.2004;
Kalia A., Bessen D.E.;
"Natural selection and evolution of streptococcal virulence involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).
EMBL; AY234128; AAP39948.1; -; Genomic_DNA.
Kinase.
SEQUENCE 440 AA; 49924 MW; D6227EF040B758DB CRC64;
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SNR; Q7X0Y2; 63-398.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator activ
GO; GO:0008243; F:protein binding; IEA.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR004093; Streptokinase.
Pfam; PF02821; Staphylokinase;
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EMBL; AY234130; AAP39950.1; -; Genomic_DNA HSSP; Q53284; 1C4P.
SMR; Q7X0Y7; 63-398.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator ac
GO; GO:0008243; F:protein binding; IEA.
InterPro; IPR008124; Streptokinase.
InterPro; IPR008124; Streptokinase.
                                                                                                                                                                                       involved in tissue-specific adaptations.";
J. Bacteriol. 186:110-121(2004).
EMBL; AY234130; AAP39950.1; -; Genomic_DNA.
HSSP; Q53284: 1C4P
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Percent Similarity:
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Query Match:
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J. Infect. Dis. 190;727-738 (2004).

EMBL; CP000003; AARB7827.1; -; Genomic_DNA
SMR; QSX976; 63-398.

GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator ac
GO; GO:0008515; F:protein binding; IEA.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR004093; Staphylokinase.
Pfam; PF02871; Staphylokinase; 3.
PRINTS; PR01753; STREPKINASE.
Complete proteome; Hydrolase; Kinase.
SEQUENCE 440 AA; 50160 MW; 1C5AF07907E
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Q5X9T6;
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25-OCT-2004
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Streptokinase (EC 3.4...).
OrderedLocusNamase-wr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MGAS10394;
PubMed=15272401; DOI=10.1086/422697;
Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.E.,
Voyich J.M., DeLeo F.R., Martin J.M., Somerville G.A., Musser J.M.;
"Progress toward characterization of the group A Streptococcus
"entagenome: complete genome sequence of a macrolide-resistant serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenēs (serotype M6). Bacteria; Firmicutes; Lactobacillales;
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Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).

Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).

EMBL; AE010107; AAL98517.1; -; Genomic_DNA.

HSSP; Q51284; 1C4P.

SNR; Q8NZA6; 63-398.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0008243; F:plasminogen activator activity; IE

GO; GO:0008243; F:protein binding; IEA.

InterPro; IPR004093; Staphylokinase.

InterPro; IPR004093; Streptokinase.

Pfam; PF02821; Staphylokinase; 3.

PRINTS; PR01753; STREPKINASE.
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QBNZA6 STRP8 PRELIMINARY; PRT;
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MEDLINS=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=spyM18_2042;
Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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SEQUENCE 440 AA; 50382 MW;
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AAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAACTTGAGAAAAGCTGACTTACTA
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93.73%
87.21%
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Matches:
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Mismatches:
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Q7X0Y3;
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
      NUCLEOTIDE SEQUENCE STRAIN=ALAB49;
                                                   Streptococcus.
NCBI_TaxID=1314;
                                                                                     Streptococcus pyogenes
Bacteria; Firmicutes;
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J. Bacteriol. 186:110-121(2004).

EMBL; AY234134; AAP39954.1; -; Genomic_DNA.

HSSP; Q53284; 1C4P.

SNR; Q7X0Y3; 63-398.

G0; G0:0016301; F:kinase activity; IEA.

G0; G0:0008243; F:plassinogen activator activ

G0; G0:0005515; F:protein binding; IEA.

InterPro; IPR004093; Staphylokinase.

InterPro; IPR008124; Streptokinase.

Pfam; PF02821; Staphylokinase; 3.

PRINTS; PR01753; STREPKINASE.
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Kalia A., Bessen D.E.;
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REMBL; AY234138; AAP39958.1; -; Genomic_DNA.
DR HSSP; Q53284; 104P.
DR SMR; Q7X0Y0; 63-398.
DR GO; GO:0016301; F:Kinase CG; GO:0008243; FC; GG; GG; GO:0008243; 
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SMR; Q7X0Y0; 63-398.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008243; F:plasminogen activator activity; IEF.
GO; GO:0008243; F:plasminogen activator activity; IEF.
InterPro; IPR004093; Staphylokinase.
InterPro; IPR004093; Staphylokinase.
Pfam; PF02821; Staphylokinase; 3.
Pfam; PF02821; Staphylokinase; 3.
PF02821; Staphylokinase; 3.
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NCBI_TaxID=1314;
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